

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 03:22:05 ; Search time 2219 Seconds
(without alignments)
18906.432 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccattgggggc.....ctctcgagatcaagttact 7992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_23Sep04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	7992	100.0	7992	6	AAL47276 Hepatitis
2	7992	100.0	10690	6	ABK91412 Hepatitis
3	7992	100.0	10690	9	ACA61697 Hepatitis
4	7992	100.0	10690	10	ADC83762 Hepatitis
5	7990.4	100.0	7992	6	AAL47281 Hepatitis
6	7990.4	100.0	10690	6	ABK91448 Hepatitis
7	7990.4	100.0	10690	6	ABK91435 Hepatitis
8	7990.4	100.0	10690	6	ABK91243 Hepatitis
9	7990.4	100.0	10690	6	ABK91434 Hepatitis
10	7990.4	100.0	11313	12	ADP86264 Hepatitis
11	7989	100.0	7989	3	AAA98968 Hepatitis
12	7989	100.0	7989	12	ADJ57845 HCV repli
13	7988.8	100.0	10690	6	ABK91440 Hepatitis
14	7988.8	100.0	11313	12	ADP86271 Hepatitis
15	7987.4	99.9	7989	6	AAL47280 Hepatitis
16	7987.2	99.9	7992	6	AAL47277 Hepatitis
17	7987.2	99.9	7992	6	AAL47277 Hepatitis
18	7987.2	99.9	11313	12	ADP86265 Hepatitis
19	7985.8	99.9	7989	6	AAD25326 Hepatitis
20	7985.6	99.9	11313	12	ADP86272 Hepatitis
21	7984	99.9	10690	6	ABK91242 Hepatitis

22	7982.6	99.9	7989	6	AAD25325 Hepatitis
23	7982.6	99.9	7989	10	ADD93734 Hepatitis
24	7982.4	99.9	11313	12	ADP86275 Hepatitis
25	7981	99.9	10691	6	ABK91423 Hepatitis
26	7980.8	99.9	11313	12	ADP86273 Hepatitis
27	7979.2	99.8	11313	12	ADP86266 Hepatitis
28	7979	99.8	10693	6	ABK91438 Hepatitis
29	7977.6	99.8	11313	12	ADP86268 Hepatitis
30	7977.4	99.8	10693	6	ABK91443 Hepatitis
31	7976.2	99.8	10691	6	ABK91439 Hepatitis
32	7975	99.8	7987	6	AAD25321 Hepatitis
33	7974.4	99.8	11313	12	ADP86267 Hepatitis
34	7973.6	99.8	7991	6	AAL47279 Hepatitis
35	7973.4	99.8	7987	6	AAD25329 Hepatitis
36	7971.8	99.7	7987	6	AAD25324 Hepatitis
37	7967	99.7	8001	3	AAA98967 Hepatitis
38	7966.2	99.7	7995	6	AAL47278 Hepatitis
39	7958.4	99.6	11313	12	ADP86270 Hepatitis
40	7955.2	99.5	11313	12	ADP86269 Hepatitis
41	7777.8	97.3	7989	10	ADD93733 Hepatitis
42	7714.4	96.5	11184	12	ADP86274 Hepatitis
43	7706.4	96.4	11184	12	ADP86276 Hepatitis
44	7701.6	96.4	11184	12	ADP86277 Hepatitis
45	7695.4	96.3	7848	6	AAD25323 Hepatitis

ALIGNMENTS

RESULT 1

AAL47276

ID AAL47276 standard; DNA; 7992 BP.

XX

AC AAL47276;

XX

DT 30-AUG-2002 (first entry)

XX

DE Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.

XX

KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis; virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX

OS Hepatitis C virus.

XX

FR Key Location/Qualifiers

FT CDS

FT 342..1181

FT /*tag= a

FT CDS

FT /*product= "core-neo fusion protein"

FT 1801..7758

FT /*tag= b

FT /*product= "NS3 proteinase/helicase"

XX

PN WO200238793-A2.

XX

PD 16-MAY-2002.

XX

PF 02-NOV-2001; 2001WO-US046350.

XX

PR 07-NOV-2000; 2000US-0245866P.

XX

PA (ANAD-) ANADYS PHARM INC.

XX

PI Bichko V;

XX

XX WPI; 2002-490082/52.

DR P-PSDB; AAO18000, AAO18001.

XX

PT Novel nucleic acid encoding replication competent recombinant hepatitis C virus genome useful for screening anti-hepatitis C virus therapeutics and for vaccine development.

XX

PS Claim 6; Page 43-47; 85pp; English.

CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement non-
CC infectious, replication-defective infection-component, and replication-
CC defective non-infectious HCV, in gene therapy or gene vaccination
CC targeted to hepatic tissue for treating an animal infected or susceptible
CC to HCV infection and for studying HCV infection and propagation. The
CC present sequence is a clone of a fragment of the HCV genome which encodes
CC the core-neo and NS3 proteinase/helicase proteins
XX
SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

Query Match		100.0%;	Score 7992;	DB 6;	Length 7992;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 7992;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	GCACGCCCCGATGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACCTACTG	60			
DB	1	GCACGCCCCGATGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACCTACTG	60			
QY	61	TCCTACGCGAAGAGCGCTAGCCATGGCGGTAGTATGATGATGATGATGATGATGATG	120			
DB	61	TCCTACGCGAAGAGCGCTAGCCATGGCGGTAGTATGATGATGATGATGATGATGATG	120			
QY	121	CCCCCTCCGGGAGAGCCATAGTGTCTGGGAAACCGGTGAGTACACCGGAAATGGCAG	180			
DB	121	CCCCCTCCGGGAGAGCCATAGTGTCTGGGAAACCGGTGAGTACACCGGAAATGGCAG	180			
QY	181	GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAATTTGGCGGTGCC	240			
DB	181	GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAATTTGGCGGTGCC	240			
QY	241	GCGAGATGCTAGCGGAGTGTGGTTCGGAAGGCTTGTGTTACTCCCTGATAGG	300			
DB	241	GCGAGATGCTAGCGGAGTGTGGTTCGGAAGGCTTGTGTTACTCCCTGATAGG	300			
QY	301	GTGCTTGGAGTGGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGAACTCTAAAC	360			
DB	301	GTGCTTGGAGTGGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGAACTCTAAAC	360			
QY	361	CTCAAGAGAAACCAAGAGCGCGCCATGATTTGAACAGATGGATTTGACGCGAGTTCTC	420			
DB	361	CTCAAGAGAAACCAAGAGCGCGCCATGATTTGAACAGATGGATTTGACGCGAGTTCTC	420			
QY	421	CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGACAATCGGCTGCT	480			
DB	421	CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGACAATCGGCTGCT	480			
QY	481	CTGATGCGCGGTTCCTGGCTGTGACGCGAGGGCGCGCGGTCTTTTGTCAAGACCG	540			
DB	481	CTGATGCGCGGTTCCTGGCTGTGACGCGAGGGCGCGCGGTCTTTTGTCAAGACCG	540			
QY	541	ACCTGTCCGGTGCCTTGAATGAATGACGAGGAGCGGCGGTATCGTGGCTGGCCA	600			
DB	541	ACCTGTCCGGTGCCTTGAATGAATGACGAGGAGCGGCGGTATCGTGGCTGGCCA	600			
QY	601	CGACGGGCGTTCCTTGGCAGCTGTGCTCGAGTTGTCTACTGAAGCGGAAGGACTGGC	660			
DB	601	CGACGGGCGTTCCTTGGCAGCTGTGCTCGAGTTGTCTACTGAAGCGGAAGGACTGGC	660			
QY	661	TGCTATTGGGCGAAGTGC CGGGCGAGGATCTCCTGTCACTCACTTGTCTCTGCGAGA	720			
DB	661	TGCTATTGGGCGAAGTGC CGGGCGAGGATCTCCTGTCACTCACTTGTCTCTGCGAGA	720			
QY	721	AAGTATCCATGCGGTGATGCAATGCGGGCTGCATACGCTTTGATCCGGCTACCTGCC	780			
DB	721	AAGTATCCATGCGGTGATGCAATGCGGGCTGCATACGCTTTGATCCGGCTACCTGCC	780			

QY	781	CATTGACCAACAAGGAAACATCGATCGAGGACGACGTACTCGATGGAAGCCGGTC	840
DB	781	CATTGACCAACAAGGAAACATCGATCGAGGACGACGTACTCGATGGAAGCCGGTC	840
QY	841	TTGTGATCAGATGATCTGGAAGAGACATCAGGGGTCGCGGCGAGCCGAATCTTTCG	900
DB	841	TTGTGATCAGATGATCTGGAAGAGACATCAGGGGTCGCGGCGAGCCGAATCTTTCG	900
QY	901	CCAGGCTCAAGGCGGCGCATGCCGAGGAGATCTCGTCTGAGCCATGGGATGCTT	960
DB	901	CCAGGCTCAAGGCGGCGCATGCCGAGGAGATCTCGTCTGAGCCATGGGATGCTT	960
QY	961	GTTGCGGAATATCATGTTGGAATGCGGCTTTCTGATTCATCGATGTGGCGGC	1020
DB	961	GTTGCGGAATATCATGTTGGAATGCGGCTTTCTGATTCATCGATGTGGCGGC	1020
QY	1021	TGGTGTGGGACCGCTATCAGGACATAGCTGTGGCTACCCGCTGATATTGCTGAAGAC	1080
DB	1021	TGGTGTGGGACCGCTATCAGGACATAGCTGTGGCTACCCGCTGATATTGCTGAAGAC	1080
QY	1081	TTGGCGGGAATGGGCTGACCGCTTCTGATGTTTACGGTATCGCGCTCCGATTCGC	1140
DB	1081	TTGGCGGGAATGGGCTGACCGCTTCTGATGTTTACGGTATCGCGCTCCGATTCGC	1140
QY	1141	AGCGATGCGCTTCTATCGCTTCTTACAGGATCTTCTGAGTTTAAACAGACCAACG	1200
DB	1141	AGCGATGCGCTTCTATCGCTTCTTACAGGATCTTCTGAGTTTAAACAGACCAACG	1200
QY	1201	GTTTCCCTCTAGCGGATCAATTCGCGCTCTCTCCCTCCCGCTTACGTTACTGGC	1260
DB	1201	GTTTCCCTCTAGCGGATCAATTCGCGCTCTCTCCCTCCCGCTTACGTTACTGGC	1260
QY	1261	CGAAGCGCTTGAATTAAGCGCGGTGCTGCTATGATTTTCCACCATTTG	1320
DB	1261	CGAAGCGCTTGAATTAAGCGCGGTGCTGCTATGATTTTCCACCATTTG	1320
QY	1321	CCGTCTTTTGGCAATGTGAGGCGCGGAACTGGCTCTGTTGACGAGATTCCT	1380
DB	1321	CCGTCTTTTGGCAATGTGAGGCGCGGAACTGGCTCTGTTGACGAGATTCCT	1380
QY	1381	AGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGAAGGAGCA	1440
DB	1381	AGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGAAGGAGCA	1440
QY	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAGTCTGAGGACCTTTGAGGAGCGG	1500
DB	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAGTCTGAGGACCTTTGAGGAGCGG	1500
QY	1501	AACCCCGCCTGCGGACAGGTGCTCTGCGGCAAAAGCCAGCTGTATAGATACACT	1560
DB	1501	AACCCCGCCTGCGGACAGGTGCTCTGCGGCAAAAGCCAGCTGTATAGATACACT	1560
QY	1561	GCAGAGGCGGCAACCCGAGTGCACAGTGTGAGTTGAGTTGAGTTGAGTTGAGTT	1620
DB	1561	GCAGAGGCGGCAACCCGAGTGCACAGTGTGAGTTGAGTTGAGTTGAGTTGAGTT	1620
QY	1621	TGGCTCTCTCAAGGCTATTCAAGGGGCTGAAGGATGCGGAGTACCCATTCG	1680
DB	1621	TGGCTCTCTCAAGGCTATTCAAGGGGCTGAAGGATGCGGAGTACCCATTCG	1680
QY	1681	ATGGGATCTGATCTGGGCTCGGTGCACATGTTTACATGTTTGTGAGTTGAGTT	1740
DB	1681	ATGGGATCTGATCTGGGCTCGGTGCACATGTTTACATGTTTGTGAGTTGAGTT	1740
QY	1741	AACGCTAGGCGGCGGCAACCCAGGAGTGTGCTTCTTCTTGAAGAAACAGATATAC	1800
DB	1741	AACGCTAGGCGGCGGCAACCCAGGAGTGTGCTTCTTCTTGAAGAAACAGATATAC	1800
QY	1801	ATGGGCGCTTATTAAGGCTTCTCCCAACAGACGCGGAGGCTTCTGCTGATCATCACT	1860
DB	1801	ATGGGCGCTTATTAAGGCTTCTCCCAACAGACGCGGAGGCTTCTGCTGATCATCACT	1860
QY	1861	AGCCTCACAGGCGGCGGACAGGAACAGGTCGAGGGGAGGTCCAGTGTGTTCTCCACGCA	1920

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QY	4081	GC	GATAGCATCACTGATGCAATTCACAGAGCTCTATCACACAGCCCGCTCAACCAACCAAT	4140
DB				
QY	4141	AC	CTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
DB				
QY	4141	AC	CTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
DB				
QY	4201	GT	TTCTCTGCTTTGATAGCGCGGCATCGTGGAGCGGTGTTGGCAGCATAGGCCCTTGGG	4260
DB				
QY	4201	GT	TTCTCTGCTTTGATAGCGCGGCATCGTGGAGCGGTGTTGGCAGCATAGGCCCTTGGG	4260
DB				
QY	4261	AA	GGTGCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCC	4320
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QY	4261	AA	GGTGCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCC	4320
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QY	4321	TT	TAAAGGTTCATAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTTAACTATCCTCTGCT	4380
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QY	4381	AT	CTCTCTCCCTGGCGCCCTAGTCTCGGGTCTGTGGCAGCGATCTATGCTCGGCAC	4440
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QY	4381	AT	CTCTCTCCCTGGCGCCCTAGTCTCGGGTCTGTGGCAGCGATCTATGCTCGGCAC	4440
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QY	4441	GT	GGGCCACAGGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGTTCCGCG	4500
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DB				
QY	4561	CA	GATCCTCTTAGTCTTACCATCACTCAGTCTGTAAGAGGCTTCAACAGTGGATCAAC	4620
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QY	4561	CA	GATCCTCTTAGTCTTACCATCACTCAGTCTGTAAGAGGCTTCAACAGTGGATCAAC	4620
DB				
QY	4621	GA	GGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680
DB				
QY	4621	GA	GGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680
DB				
QY	4681	AC	GGTGTGACTGAATTAAGACCTGGCTCCAGTCCAGCTCCGCGGATTCGCGGGA	4740
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QY	4741	GT	CCCCCTCTCTCATGTCAAGTGGGTACAGGGAGTCTGGCGGGCGAGCGGATCATG	4800
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QY	4861	AT	CGTGGGGCTTAGGACCTGTAGTAAACGTTGAGCATGGAACATTCGCCATTAACCGTAC	4920
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QY	4861	AT	CGTGGGGCTTAGGACCTGTAGTAAACGTTGAGCATGGAACATTCGCCATTAACCGTAC	4920
DB				
QY	4921	AC	ACGGCCCCCTGCAAGCTTCCCGCGCCAAATTTATCTAGGGCGCTGTGGCGGGTG	4980
DB				
QY	4921	AC	ACGGCCCCCTGCAAGCTTCCCGCGCCAAATTTATCTAGGGCGCTGTGGCGGGTG	4980
DB				
QY	4981	GT	GCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTTCACTACGTGACGGCGATG	5040
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QY	4981	GT	GCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTTCACTACGTGACGGCGATG	5040
DB				
QY	5041	AC	CACTGAACAGTAAAGTGGCGGTGACGGTTCGGCCCCCGAATTTCTTCAAGAGTG	5100
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QY	5041	AC	CACTGAACAGTAAAGTGGCGGTGACGGTTCGGCCCCCGAATTTCTTCAAGAGTG	5100
DB				
QY	5101	GAT	GGGTGCGGTTTGCAAGGTAAGTTCAGGTTCCAGGTTCCAGGTTCCAGGAGGAGGTC	5160
DB				
QY	5101	GAT	GGGTGCGGTTTGCAAGGTAAGTTCAGGTTCCAGGTTCCAGGTTCCAGGAGGAGGTC	5160
DB				
QY	5161	AC	ATTCTCTGTCGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATTCGAGAGCCGAA	5220
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QY	5161	AC	ATTCTCTGTCGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATTCGAGAGCCGAA	5220
DB				
QY	5221	CC	GAGCTAGCAGTGTCTACTTCCATGCTCACGACCCCTCCACATTAAGCGGAGAGCG	5280
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QY	5221	CC	GAGCTAGCAGTGTCTACTTCCATGCTCACGACCCCTCCACATTAAGCGGAGAGCG	5280
DB				
QY	5281	GT	TAAAGCTAGGCTGGCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
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FT	misc_signal	1190..1800		QY	181	GACGACCGGGTCTCTTTCTTTGGATCAACCCGCTCAATGCTCGAGATTTCGGCGTGC	240
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FT		/note= "Plasmid derived sequences"		Db	361	CTCAAGAAAAACCAAAAGGCGCGCATGATTGAAACAAGATGGATTGCACGCGATTCTC	420
FT	WO200259321-A2.						
XX	01-AUG-2002.			QY	421	CGGCGCTGGGTGGAGAGCTATTGGCTATGCTGGGCACACACACATGGCTGCT	480
XX				Db	421	CGGCGCTGGGTGGAGAGCTATTGGCTATGCTGGGCACACACACATGGCTGCT	480
XX	16-JAN-2002; 2002WO-EP000526.						
XX	23-JAN-2001; 2001US-0263479P.			QY	481	CTGATGCCGCGTGTTCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG	540
XX	(RICE-) 1ST RICERCHE BIOL MOLECOLARE ANGELETTI.			Db	481	CTGATGCCGCGTGTTCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG	540
XX	De Francesco R, Migliaccio G, Paonessa G;			QY	541	ACCTGTCCGCTGCTGAAATGAATGAGGACGAGGCGCGGCTATCTGCTGCGTGC	600
XX	WPI; 2002-599793/64.			Db	541	ACCTGTCCGCTGCTGAAATGAATGAGGACGAGGCGCGGCTATCTGCTGCGTGC	600
XX	New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV			QY	601	CGACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGACCTGGC	660
XX	NS5 encoding region, or encephalomyocarditis virus (EMCV) internal			Db	601	CGACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGACCTGGC	660
XX	ribosome entry site (IRES) region, useful in studying HCV replication and						
XX	expression.			QY	661	TGCTATTGGCGAAGTGCCTGGCGCAGGATCTCTCTGTCTCATCTCACCTTCTCTG	720
XX	Claim 1; Fig 1; 69pp; English.			Db	661	TGCTATTGGCGAAGTGCCTGGCGCAGGATCTCTCTGTCTCATCTCACCTTCTCTG	720
XX	The invention relates to nucleic acid molecules comprising altered HCV			QY	721	AAGTATCCATCATCGCTGATGCAATGCGCGCTGCTACGCTTGATCCGGCTACCTGCC	780
XX	NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)			Db	721	AAGTATCCATCATCGCTGATGCAATGCGCGCTGCTACGCTTGATCCGGCTACCTGCC	780
XX	internal ribosome entry site (IRES) region coding for one or more NS3,						
XX	NSSA, or EMCV IRES mutations, respectively. The location of the mutations			QY	781	CATTGACACCAAGCGAATCATCGATCGAGCGAGCAGTACTCGGATGGAAGCGGCTC	840
XX	are detailed in the specification. Also included are (1) an expression			Db	781	CATTGACACCAAGCGAATCATCGATCGAGCGAGCAGTACTCGGATGGAAGCGGCTC	840
XX	vector comprising a nucleotide sequence coding for the altered nucleic						
XX	acids, which is transcriptionally coupled to an exogenous promoter; (2) a			QY	841	TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCAGCGAATCTGTCG	900
XX	recombinant cell human hepatoma cell comprising the altered nucleic acids			Db	841	TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCAGCGAATCTGTCG	900
XX	; (3) a recombinant cell produced by introducing into a human hepatoma						
XX	cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)			QY	901	COAGCTCAAGCGCGCATGCGCGGAGGATCTGCTGCGTGAACCATGCGATGCT	960
XX	replicon enhanced cell or which containing a functional HCV replicon; (5)			Db	901	COAGCTCAAGCGCGCATGCGCGGAGGATCTGCTGCGTGAACCATGCGATGCT	960
XX	an HCV replicon enhanced cells made in the method; and (6) measuring the						
XX	ability of a compound to affect HCV activity. The HCV replicons and HCV			QY	961	GCTTCCGCAATATCATGTGGAAATGCCGCTTTCTTGATTCATCGACTGTGGCGGCG	1020
XX	replicon enhanced cells are useful in studying HCV replication and			Db	961	GCTTCCGCAATATCATGTGGAAATGCCGCTTTCTTGATTCATCGACTGTGGCGGCG	1020
XX	expression, and HCV and host cell interactions, producing HCV RNA and						
XX	proteins, and providing a system for measuring the ability of a compound			QY	1021	TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTGCTGAAGAC	1080
XX	to modulate one or more HCV activities e.g. to discover drugs which may			Db	1021	TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTGCTGAAGAC	1080
XX	treat HCV mediated diseases such as liver failure, cirrhosis and						
XX	hepatocellular carcinoma. The present sequence is the HCV based vector			QY	1081	TTGGCGGGAATGGGCTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTCCG	1140
XX	pHCVNeo.17, used as a basis for the adaptive mutations of the invention			Db	1081	TTGGCGGGAATGGGCTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTCCG	1140
XX	Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;						
XX	Query Match 100.0%; Score 7992; DB 6; Length 10690;			QY	1141	ACGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTTGAGTTTAAACAGACCAACAG	1200
XX	Best Local Similarity 100.0%; Pred. No. 0;			Db	1141	ACGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTTGAGTTTAAACAGACCAACG	1200
XX	Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	GCACGCCCGGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60				
Db	1	GCACGCCCGGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60				
QY	61	TCTTACGACAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC	120				
Db	61	TCTTACGACAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC	120				
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCAGTGTAGTACACCGAATGCCAG	180				
Db	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCAGTGTAGTACACCGAATGCCAG	180				

QY 1261 CGAAGCGCTTGAATAAGCCCGGTGTGCGTTTGTCTATATATATATTTTCCACCATATTG 1320
DB 1261 CGAAGCGCTTGAATAAGCCCGGTGTGCGTTTGTCTATATATATATTTTCCACCATATTG 1320
QY 1321 CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTCTTGTGACGACATTCCT 1380
DB 1321 CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTCTTGTGACGACATTCCT 1380
QY 1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGTCTGTGAAGGAAGCA 1440
DB 1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGTCTGTGAAGGAAGCA 1440
QY 1441 GTTCTCTCTGGAAGCTCTTTGAAGACAAACAAAGTCTGTGAGGACCCCTTTGCAGGACGCG 1500
DB 1441 GTTCTCTCTGGAAGCTCTTTGAAGACAAACAAAGTCTGTGAGGACCCCTTTGCAGGACGCG 1500
QY 1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCCAAAGCCACGGTGTATAAGATACACCT 1560
DB 1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCCAAAGCCACGGTGTATAAGATACACCT 1560
QY 1561 GCAAGGGGCGCAAAACCCAGTGCACAGTGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
DB 1561 GCAAGGGGCGCAAAACCCAGTGCACAGTGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCCAGAGTACCCCATTTG 1680
DB 1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCCAGAGTACCCCATTTG 1680
QY 1681 ATGGATCTGATCTGGGCGCTCGGTGCAATCTTTTACATGTGTTTGTGAGGTTTAAA 1740
DB 1681 ATGGATCTGATCTGGGCGCTCGGTGCAATCTTTTACATGTGTTTGTGAGGTTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGCAACCAAGGGGACGTGTTTCTTTGAAAAACAGATAATACC 1800
DB 1741 AACGTCTAGGCCCCCGCAACCAAGGGGACGTGTTTCTTTGAAAAACAGATAATACC 1800
QY 1801 ATGGGCGCTATTACGGCTACTTCCAAACAGAGCGGAGGCTTCTGGCTGATCATCACT 1860
DB 1801 ATGGGCGCTATTACGGGCTACTTCCAAACAGAGCGGAGGCTTCTGGCTGATCATCACT 1860
QY 1861 AGCTCTACAGGCGGGACAGGAACAGGTCTGAGGGGAGGTCGAAGTGTCTTCAACGCA 1920
DB 1861 AGCTCTACAGGCGGGACAGGAACAGGTCTGAGGGGAGGTCGAAGTGTCTTCAACGCA 1920
QY 1921 ACACAACTTTCTTGGGACCTGCGTCAATGGCGGTGTGTGGACTGTCTATCATGTGTC 1980
DB 1921 ACACAACTTTCTTGGGACCTGCGTCAATGGCGGTGTGTGGACTGTCTATCATGTGTC 1980
QY 1981 GGCTCAAGACCTTGTGCGGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGGAC 2040
DB 1981 GGCTCAAGACCTTGTGCGGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGAAGCGCCCGCGGGCGGTCTTGGACTGTCTATCATGTGTC 2100
DB 2041 CAGGACCTCGTGGCTGGAAGCGCCCGCGGGCGGTCTTGGACTGTCTATCATGTGTC 2100
QY 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGCATGCCGATGTCTTCTTGAAGGGCTCTTCG 2160
DB 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGCATGCCGATGTCTTCTTGAAGGGCTCTTCG 2160
QY 2161 GGCAGACAGGGGAGGAGCTTCTTCCCGCAGGCGGTCTTCTTGAAGGGCTCTTCG 2220
DB 2161 GGCAGACAGGGGAGGAGCTTCTTCCCGCAGGCGGTCTTCTTGAAGGGCTCTTCG 2220
QY 2221 GGCAGCTCGTCTGCTTCCCTCGGGGACGCTGTGGGATCTTTTGGGCTGCGGTGTC 2280
DB 2221 GGCAGCTCGTCTGCTTCCCTCGGGGACGCTGTGGGATCTTTTGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTGCGAAGGGGTGGAATTTGTATCCCGTCTGAGTCTATGGAAACCACTATG 2340
DB 2281 ACCGAGGGGTGCGAAGGGGTGGAATTTGTATCCCGTCTGAGTCTATGGAAACCACTATG 2340
QY 2341 CGGTCCCGGTCTTACGGGACAACTCGTCCCTCCGCGGTACCGGACAGACATTTCCAGGTG 2400

DB 2341 CGGTCCCGGTCTTACGGGACAACTCGTCCCTCCGCGGTACCGGACATTTCCAGGTG 2400
QY 2401 GCCCATCTACAGCCCTTACTGCTAGCGGCAAGAGACACTAAGGTGCGGCTGCTGATGCA 2460
DB 2401 GCCCATCTACAGCCCTTACTGCTAGCGGCAAGAGACACTAAGGTGCGGCTGCTGATGCA 2460
QY 2461 GCCCAAGGGTATAAGGTGCTTCTGCTGAACCCGCTCGTCCGCGCCACCTTAGTTCGGG 2520
DB 2461 GCCCAAGGGTATAAGGTGCTTCTGCTGAACCCGCTCGTCCGCGCCACCTTAGTTCGGG 2520
QY 2521 GGGTATATCTTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAAAGGACATC 2580
DB 2521 GGGTATATCTTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAAAGGACATC 2580
QY 2581 ACCAGGGTGCCTTACCTACCTTCCACCTATGGAAGTTCCTTGGCCAGCGTGTGTC 2640
DB 2581 ACCAGGGTGCCTTACCTACCTTCCACCTATGGAAGTTCCTTGGCCAGCGTGTGTC 2640
QY 2641 TCTGGGGGGCTTATGACATCATATATATGATGATGCTCAACTGACTCGACCACT 2700
DB 2641 TCTGGGGGGCTTATGACATCATATATATGATGATGCTCAACTGACTCGACCACT 2700
QY 2701 ATCTTGGGCTCGGCACAGTCTGACCAAGCGGAGAGCGGCTGGAGCGGCTGCTGTC 2760
DB 2701 ATCTTGGGCTCGGCACAGTCTGACCAAGCGGAGAGCGGCTGGAGCGGCTGCTGTC 2760
QY 2761 CTGCGCACCGCTACGCTTCCGGGATCGGTCACTGCGCACATCCAAACATCGAGGAGGTG 2820
DB 2761 CTGCGCACCGCTACGCTTCCGGGATCGGTCACTGCGCACATCCAAACATCGAGGAGGTG 2820
QY 2821 GCTCTGTCCAGCTTGGAGAAATCCCTTTTATGCGCAAGGCCATCCCATCGAGACCACT 2880
DB 2821 GCTCTGTCCAGCTTGGAGAAATCCCTTTTATGCGCAAGGCCATCCCATCGAGACCACT 2880
QY 2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGTCTGCGCGG 2940
DB 2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGTCTGCGCGG 2940
QY 2941 AAGTGTCCGCGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGTATGATCCGTC 3000
DB 2941 AAGTGTCCGCGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGTATGATCCGTC 3000
QY 3001 ATACCACTAGCGGAGAGCTCATTTGCTAGCAACGCGCTCTAATGACGGGCTTTACC 3060
DB 3001 ATACCACTAGCGGAGAGCTCATTTGCTAGCAACGCGCTCTAATGACGGGCTTTACC 3060
QY 3061 GGCATTTCCGACTCAGTGTGACTGCAATACATGTGTACCCAGAGAGTCTGACG 3120
DB 3061 GGCATTTCCGACTCAGTGTGACTGCAATACATGTGTACCCAGAGAGTCTGACG 3120
QY 3121 CTGACCCGACCTTCAACATGAGACGACCGCTGCGCAACAGCGGGTGTACGCTCG 3180
DB 3121 CTGACCCGACCTTCAACATGAGACGACCGCTGCGCAACAGCGGGTGTACGCTCG 3180
QY 3181 CAGCGGAGGAGGAGCTGTTAGGGGAGGATGGGCAATTAAGTGTGACTTCCAGGA 3240
DB 3181 CAGCGGAGGAGGAGCTGTTAGGGGAGGATGGGCAATTAAGTGTGACTTCCAGGA 3240
QY 3241 GAACGGGCTTGGGCAATGTTTCGATTCCTCGGCTGCTGCGAGTGTATGACGGGCTGT 3300
DB 3241 GAACGGGCTTGGGCAATGTTTCGATTCCTCGGCTGCTGCGAGTGTATGACGGGCTGT 3300
QY 3301 GCTTGTGACGAGTCAAGCGGCGGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
DB 3301 GCTTGTGACGAGTCAAGCGGCGGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
QY 3361 CCAGGGTGTGCGGCTGCTGCGGAGGACCTTGGAGTCTCTGGGAGAGCGCTTTTACAGGCTC 3420
DB 3361 CCAGGGTGTGCGGCTGCTGCGGAGGACCTTGGAGTCTCTGGGAGAGCGCTTTTACAGGCTC 3420
QY 3421 ACCACATAGACGCCCATTTCTTGTCCGACACTAAGCAGGCGGAGACATTTCCCTAC 3480

Db	3421	ACCCATAGACGCCCATTTCTGTCCAGACTAAGCAGGACAGACAACATTCCTCCCTAC	3480	QY	4561	CAGATCCTCTCTAGTCTTACCATCACTAGCTGCTGAAGAGGCTTCACAGTGGATCAAC	4620
QY	3481	CTGGTAGCATACAGGCTACGGTGTGGCCAGGCTCAGGCTCCACTCCATCGTGGAC	3540	Db	4561	CAGATCCTCTCTAGTCTTACCATCACTAGCTGCTGAAGAGGCTTCACAGTGGATCAAC	4620
Db	3481	CTGGTAGCATACAGGCTACGGTGTGGCCAGGCTCAGGCTCCACTCCATCGTGGAC	3540	QY	4621	GAGGACTGTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
QY	3541	CAAACTGGGAAGTGTCTCAFAAGCTTAAAGCCTACGCTGCACGGGCCAACGCCCTCGCTG	3600	Db	4621	GAGGACTGTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
Db	3541	CAAACTGGGAAGTGTCTCAFAAGCTTAAAGCCTACGCTGCACGGGCCAACGCCCTCGCTG	3600	QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGANTTCCGGGA	4740
QY	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTATACACACACACCCCATAAACAAATACATC	3660	Db	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGANTTCCGGGA	4740
Db	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTATACACACACACCCCATAAACAAATACATC	3660	QY	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGACGCGCATCATG	4800
QY	3661	ATGGCATGTCTGGCTGACCTGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGGGA	3720	Db	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGACGCGCATCATG	4800
Db	3661	ATGGCATGTCTGGCTGACCTGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGGGA	3720	QY	4801	CAAAACACCTGCCCATGTGGAGCACAGATCACCGGACATGTGAAGAACGCTTCCATGAGG	4860
QY	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCTGACAAACAGGACGCTGGTCAATTGTGGGCAGG	3780	Db	4801	CAAAACACCTGCCCATGTGGAGCACAGATCACCGGACATGTGAAGAACGCTTCCATGAGG	4860
Db	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCTGACAAACAGGACGCTGGTCAATTGTGGGCAGG	3780	QY	4861	ATCGTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTTCCCATTAACGCGTAC	4920
QY	3781	ATCATCTTGTCCGAAAGCCGCCATCATTCGCCACAGGGAAGTCTTTTACCGGGAGTTC	3840	Db	4861	ATCGTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTTCCCATTAACGCGTAC	4920
Db	3781	ATCATCTTGTCCGAAAGCCGCCATCATTCGCCACAGGGAAGTCTTTTACCGGGAGTTC	3840	QY	4921	ACCAAGGGCCCTGCAACGCCCTCCCGCGGCCAAATTTATTTCTAGGGCGCTGTGGCGGTG	4980
QY	3841	GATGAGATGGAAGTGGCCCTCACACTCCCTTACATCGAACAGGGAATGCAGCTCGCC	3900	Db	4921	ACCAAGGGCCCTGCAACGCCCTCCCGCGGCCAAATTTATTTCTAGGGCGCTGTGGCGGTG	4980
Db	3841	GATGAGATGGAAGTGGCCCTCACACTCCCTTACATCGAACAGGGAATGCAGCTCGCC	3900	QY	4981	GCTGCTGAGGAGTACGTGGAGTTACGCGGCTGGGGATTTCCACTAGTACGCGGCATG	5040
QY	3901	GAACAATTCAAACAGAGGCAATCGGTTGCTGCAACAGCACCAAGCAAGCGAGGCT	3960	Db	4981	GCTGCTGAGGAGTACGTGGAGTTACGCGGCTGGGGATTTCCACTAGTACGCGGCATG	5040
Db	3901	GAACAATTCAAACAGAGGCAATCGGTTGCTGCAACAGCACCAAGCAAGCGAGGCT	3960	QY	5041	ACCACTGACAACTGAAAGTGCCTGTGAGGTTCCGGCCCGGAAATTTCTTACAGAAAGTG	5100
QY	3961	GCTGCTCCGTTGGTGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGAGGCGAAGCATG	4020	Db	5041	ACCACTGACAACTGAAAGTGCCTGTGAGGTTCCGGCCCGGAAATTTCTTACAGAAAGTG	5100
Db	3961	GCTGCTCCGTTGGTGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGAGGCGAAGCATG	4020	QY	5101	GATGGGTGCGGTGTCACAGTAGCTCCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5160
QY	4021	TGGAATTCAGAGGAGATCAATATTTAGCAGGCTTGTCCACTCTGCTGGCAACCCC	4080	Db	5101	GATGGGTGCGGTGTCACAGTAGCTCCAGCTGCAAAACCCCTCTACGGGAGGAGTGC	5160
Db	4021	TGGAATTCAGAGGAGATCAATATTTAGCAGGCTTGTCCACTCTGCTGGCAACCCC	4080	QY	5161	ACATTTCTGCTGGCTCAATACATACCTGTGGTCAACAGCTCCCATGGAGCCGAA	5220
QY	4081	GGATAGCATCACTGATGGCAATTCACAGCTTATCAACAGCCGCTCAGCACCCACAT	4140	Db	5161	ACATTTCTGCTGGCTCAATACATACCTGTGGTCAACAGCTCCCATGGAGCCGAA	5220
Db	4081	GGATAGCATCACTGATGGCAATTCACAGCTTATCAACAGCCGCTCAGCACCCACAT	4140	QY	5221	CCGAGCTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATTTACGGCGGAGAG	5280
QY	4141	ACCCCTCTGTTTAAACATCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200	Db	5221	CCGAGCTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATTTACGGCGGAGAG	5280
Db	4141	ACCCCTCTGTTTAAACATCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200	QY	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
QY	4201	GCTTCTGCTTTCTGAGGCGCCGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Db	4201	GCTTCTGCTTTCTGAGGCGCCGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	QY	5341	CTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGCTCATGCTCCCGGAGCGTAC	5400
QY	4261	RAAGTGTCTTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGGCGCTCTGTGGCC	4320	Db	5341	CTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGCTCATGCTCCCGGAGCGTAC	5400
Db	4261	RAAGTGTCTTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGGCGCTCTGTGGCC	4320	QY	5401	CTCATCGAGGCCAACCTCTGTGGCGGAGGAGATGGGCGGGAACATACCCCGCTGGAG	5460
QY	4321	TTTAAAGTTCATGAGCGCGGATGTCCTCAACGAGGACCTGGTTAAACCTACTCCCTGCT	4380	Db	5401	CTCATCGAGGCCAACCTCTGTGGCGGAGGAGATGGGCGGGAACATACCCCGCTGGAG	5460
Db	4321	TTTAAAGTTCATGAGCGCGGATGTCCTCAACGAGGACCTGGTTAAACCTACTCCCTGCT	4380	QY	5461	TCAGAAATTAAGGTAGTAAATTTTGAATCTTTTGAAGCTTTTGAAGCTTTTGAAGCTTTT	5520
QY	4381	ATCCTCTCCCTGGCGGCTGCTGCGGGGTGCTGCGGAGCTGCTGCGGAGGAGGATGAG	4440	Db	5461	TCAGAAATTAAGGTAGTAAATTTTGAATCTTTTGAAGCTTTTGAAGCTTTTGAAGCTTTT	5520
Db	4381	ATCCTCTCCCTGGCGGCTGCTGCGGGGTGCTGCGGAGCTGCTGCGGAGGAGGATGAG	4440	QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCTGCGAGGTCCTGCGAGGTCCAGGAAATTCCT	5580
QY	4441	GTGGGCGCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGATAGCGTTGGCTTCCGCG	4500	Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCTGCGAGGTCCTGCGAGGTCCAGGAAATTCCT	5580
Db	4441	GTGGGCGCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGATAGCGTTGGCTTCCGCG	4500	QY	5581	CCCATATGGGACCGCCCGGATTAACACCTTCACTGTTAGAGTCTTGGAGGACCCGGAC	5640
QY	4501	GGTAAACACCTCTCCCGGAGTATGCTGAGAGGACGCTCAGCAGCGTGCAT	4560	Db	5581	CCCATATGGGACCGCCCGGATTAACACCTTCACTGTTAGAGTCTTGGAGGACCCGGAC	5640
Db	4501	GGTAAACACCTCTCCCGGAGTATGCTGAGAGGACGCTCAGCAGCGTGCAT	4560				

Db 661 TGCTATTGGCGAAGTGC CGGGG CAGGATCTCTCTGT CATCTCACTTGTCTCTCCCGAGA 720
QY 721 AAGTATCCATATGCTGTATGCAATGCGCGGTGTCATACGCTTGATCCGGCTACCTGCC 780
Db 721 AAGTATCCATATGCTGTATGCAATGCGCGGTGTCATACGCTTGATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACGACGCAATCGCATCGAGAGAGCAGTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACGACGCAATCGCATCGAGAGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGCGCAGCGAATGTTGC 900
Db 841 TTGTGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGCGCAGCGAATGTTGC 900
QY 901 CAGGCTCAAGGCGCGATGCCGAGAGGATCTCTGTCGAGCCATGCGGATGTCCT 960
Db 901 CAGGCTCAAGGCGCGATGCCGAGAGGATCTCTGTCGAGCCATGCGGATGTCCT 960
QY 961 GCTTGCAGATATCATGGTGGAAATGGCGCTTTTCTGATTCATCGACTGTGGCGGC 1020
Db 961 GCTTGCAGATATCATGGTGGAAATGGCGCTTTTCTGATTCATCGACTGTGGCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGCTACCGTGATATGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGCTACCGTGATATGCTGAAGAGC 1080
QY 1081 TTGGCGGCGAATGGGTGACCGCTTCTCGTCTTACCGGTATCGCGCTCCCGATTGCG 1140
Db 1081 TTGGCGGCGAATGGGTGACCGCTTCTCGTCTTACCGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATGCGCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGCATCGCTTCTATGCGCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTTACCACTATG 1320
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTTACCACTATG 1320
QY 1261 CGAAGCCCTTGGAAATAGGCGGTGCGTTGTCTATATGTTATTTTCAACCAATG 1320
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Db 1441 GTTCTCTGGAAGTCTTGAAGCAAAACAAACGTCGTAGCAGCCCTTTGAGGACGCG 1500
QY 1501 AACCCCCACTGCGGACAGTGCCTCTGGCCCAAAAGCCAGTGTATAGATPACCT 1560
Db 1501 AACCCCCACTGCGGACAGTGCCTCTGGCCCAAAAGCCAGTGTATAGATPACCT 1560
QY 1561 GCAAGCGGCAAAACCCAGTGCAGTGTGAGTTGAGTGTGGAAAGAGTCAAA 1620
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QY 1621 TGGCTCTCTCTCAAGCGTATTCAAAGGGCTGAAGGATGCCAGAGGTACCCCATGT 1680
Db 1621 TGGCTCTCTCTCAAGCGTATTCAAAGGGCTGAAGGATGCCAGAGGTACCCCATGT 1680
QY 1681 ATGGATCTGATCTGGGCTCGTGCATGCTTTTACATGTTTGTAGTTCAGGTTAAAA 1740
Db 1681 ATGGATCTGATCTGGGCTCGTGCATGCTTTTACATGTTTGTAGTTCAGGTTAAAA 1740
QY 1741 AACGTCTAGGCCCCCGAACCAGGCGAGTGTCTTTTCTTTTCAAAAACAGTATACC 1800
Db 1741 AACGTCTAGGCCCCCGAACCAGGCGAGTGTCTTTTCTTTTCAAAAACAGTATACC 1800

QY 1801 ATGGCGCTATTATGCGGCTACTCCAAACAGACGAGGCTTACTTGGTGCATCATCACT 1860
Db 1801 ATGGCGCTATTATGCGGCTACTCCAAACAGACGAGGCTTACTTGGTGCATCATCACT 1860
QY 1861 AGCTCACAGCGCGGACAGAAACCGAGTTCGAGGGGAGTCCAAAGTGGTCTCCACCGCA 1920
Db 1861 AGCTCACAGCGCGGACAGAAACCGAGTTCGAGGGGAGTCCAAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAATCTTTCTGCGACCTCGCTCAATGGCGTGTGTGGACTGCTCATCATGTGCG 1980
Db 1921 ACACAATCTTTCTGCGACCTCGCTCAATGGCGTGTGTGGACTGCTCATCATGTGCG 1980
QY 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
Db 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
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Db 2041 CAGGACCTCGTGGCTGGCAAGGCGCCCGCGGGCGGTTCTTGACACCATGCCTGC 2100
QY 2101 GGCGCTCGGACCTTTTACTTGTTCAGAGGCAATGCCGATGTCATTCGGTGCAGCGCGG 2160
Db 2101 GGCGCTCGGACCTTTTACTTGTTCAGAGGCAATGCCGATGTCATTCGGTGCAGCGCGG 2160
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Db 2161 GGCGACAGCAGGGGAGCGCTACTCTCCCGAGCGCGCTCTCTACTTTGAAGGCTCTCG 2220
QY 2221 GGCGCTCGACCTCTGCGGCTCGGGGCAAGTGTGGGCACTTTTGGGCTGCGGTGTC 2280
Db 2221 GGCGCTCGACCTCTGCGGCTCGGGGCAAGTGTGGGCACTTTTGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTGCAAGGCGGTGACTTTGTACCGCTCGAGTCTATCGAAGCACTATG 2340
Db 2281 ACCGAGGGGTTGCAAGGCGGTGACTTTGTACCGCTCGAGTCTATCGAAGCACTATG 2340
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Db 2341 CGGTCCCGGCTTCAACGGAACAACCTCGTCCCTCGCGCGGTACCGAGACATTCAGGTG 2400
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Db 2401 GCCCATCTACAGCGCCCTTACTGTAGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
QY 2461 GCCCAAGGTATAAGGTGCTGTCTGAAACCGCTCGTCCCGGCAACCTTACTAGTTCGG 2520
Db 2461 GCCCAAGGTATAAGGTGCTGTCTGAAACCGCTCGTCCCGGCAACCTTACTAGTTCGG 2520
QY 2521 GCGTATATGCTAAGGCACATGCTATCGACCTTAAACATCAGAACCGGGGTAGGACCATC 2580
Db 2521 GCGTATATGCTAAGGCACATGCTATCGACCTTAAACATCAGAACCGGGGTAGGACCATC 2580
QY 2581 ACCAGGCTGCCCGCATCAGTACTCAACCTATGCGCAAGTTTCTGCCGAGGTGTC 2640
Db 2581 ACCAGGCTGCCCGCATCAGTACTCAACCTATGCGCAAGTTTCTGCCGAGGTGTC 2640
QY 2641 TCTGGGGCGCTTATGACATCAATATATGATGAGTGCACCTCACTGACTGACCACT 2700
Db 2641 TCTGGGGCGCTTATGACATCAATATATGATGAGTGCACCTCACTGACTGACCACT 2700
QY 2701 ATCTGGGCAATCGGCAAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTGTCGTG 2760
Db 2701 ATCTGGGCAATCGGCAAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTGTCGTG 2760
QY 2761 CTCGCCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG 2820
Db 2761 CTCGCCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG 2820
QY 2821 GCTCTGTCCGACACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC 2880
Db 2821 GCTCTGTCCGACACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC 2880

Db 301 GTGCTTGCAGTGCCTCGGAGGTCTCGTAGACCGTGACATGAGCACGAATCCTAAAC 360
QY 361 CTCAGAGAAAAACAAGGGCGCGCATGATGAACAAGATGGATTCGACGCGAGTTCTC 420
Db 361 CTCAGAGAAAAACAAGGGCGCGCATGATGAACAAGATGGATTCGACGCGAGTTCTC 420
QY 421 CGGCCGCTTGGGTGGAGAGCTATTGGCTATGACTGAGTGGGCAACAAGCAATCGGCTGCT 480
Db 421 CGGCCGCTTGGGTGGAGAGCTATTGGCTATGACTGAGTGGGCAACAAGCAATCGGCTGCT 480
QY 481 CTGATGCCGCGGTGTTCCGCTCTGACGCGAGGGGCGCGGCTTCTTTTGTCAAGACCG 540
Db 481 CTGATGCCGCGGTGTTCCGCTCTGACGCGAGGGGCGCGGCTTCTTTTGTCAAGACCG 540
QY 541 ACTGTCCGGTCCCTGAATGAATCTGAGGACGAGCGCGCTATCGTGGCTGGCCA 600
Db 541 ACTGTCCGGTCCCTGAATGAATCTGAGGACGAGCGCGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGCGTTCCTTTCGCGAGCTGTGCTCGAGTGTGTCACTGAAGCGGGAAGGACTGCG 660
Db 601 CGACGGGCGTTCCTTTCGCGAGCTGTGCTCGAGTGTGTCACTGAAGCGGGAAGGACTGCG 660
QY 661 TGCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGATCTCACCTTGTCTCCGCGGAGA 720
Db 661 TGCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGATCTCACCTTGTCTCCGCGGAGA 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTTGTATCCGGCTACTGCG 780
Db 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTTGTATCCGGCTACTGCG 780
QY 781 CATTCGACCAACAAGCGAAACATCCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACAAGCGAAACATCCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATPAGGATGATCTGACGAAGAGCATCAGGGCTCGCGCCAGCGAAGCTGTTGC 900
Db 841 TTGTGATPAGGATGATCTGACGAAGAGCATCAGGGCTCGCGCCAGCGAAGCTGTTGC 900
QY 901 CCAGGCTCAAGGCGGATGCTCGACGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
Db 901 CCAGGCTCAAGGCGGATGCTCGACGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
QY 961 GCTTCCGCAATCATGCTGGAATGCGCGCTTTCTGGAATCATGCACTGTGCGCGGC 1020
Db 961 GCTTCCGCAATCATGCTGGAATGCGCGCTTTCTGGAATCATGCACTGTGCGCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC 1080
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTGTGTTTACGGTATCGCGCTCCCGATTGCG 1140
Db 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTGTGTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTTTAAACAGACACAAG 1200
Db 1141 AGCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTTTAAACAGACACAAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTCTACAGTCTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTCTACAGTCTACTGCG 1260
QY 1261 CGAAGCGGCTTGAATAAGGCGGCTGCGCTTTGTCTATATGTTATTTTCCACCATTTG 1320
Db 1261 CGAAGCGGCTTGAATAAGGCGGCTGCGCTTTGTCTATATGTTATTTTCCACCATTTG 1320
QY 1321 CGCTCTTTTGGCAATGTAGGGCCCGGAACCTGGCGCTGTCTTGTGACGAGCATTCCT 1380
Db 1321 CGCTCTTTTGGCAATGTAGGGCCCGGAACCTGGCGCTGTCTTGTGACGAGCATTCCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGATCTGCTGAAGGAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGATCTGCTGAAGGAGCA 1440

QY 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAACGTCGTGTAGCGACCTTTTGAGGACGGG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAACGTCGTGTAGCGACCTTTTGAGGACGGG 1500
QY 1501 AACCCGCCACTCGGCGACAGGTGCTCTGGGCCAAAAGCCAGTGTATAGATACACCT 1560
Db 1501 AACCCGCCACTCGGCGACAGGTGCTCTGGGCCAAAAGCCAGTGTATAGATACACCT 1560
QY 1561 GAAAGCGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTTGGAAAAGAGTCAAA 1620
Db 1561 GAAAGCGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTTGGAAAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGTTAAAA 1740
Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGTTAAAA 1740
QY 1741 AACGTCTAGGCCCCCGAACCACGCGGAGCTGGTTTCTTTTGA AAAACACGATATACC 1800
Db 1741 AACGTCTAGGCCCCCGAACCACGCGGAGCTGGTTTCTTTTGA AAAACACGATATACC 1800
QY 1801 ATGGCGCTATTACGGCTACTTCCAAAGAGCGGAGGCTACTTGGTGCATCATCACT 1860
Db 1801 ATGGCGCTATTACGGCTACTTCCAAAGAGCGGAGGCTACTTGGTGCATCATCACT 1860
QY 1861 AGCTTCACAGCGCGGACAGGAACAGGTGCGAGGGGAGGTCGAAGTGGTCTCCACCGCA 1920
Db 1861 AGCTTCACAGCGCGGACAGGAACAGGTGCGAGGGGAGGTCGAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAACTTTTCTGGCGACCTGCTCAATGGCGTGTGTGAGTGTCTATCATGCTGCC 1980
Db 1921 ACACAACTTTTCTGGCGACCTGCTCAATGGCGTGTGTGAGTGTCTATCATGCTGCC 1980
QY 1981 GGCTCAAGAACCTTTGCGGCCCAAAGGGCCCAATCACCCAAATGTACCAATGTGGAC 2040
Db 1981 GGCTCAAGAACCTTTGCGGCCCAAAGGGCCCAATCACCCAAATGTACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGGCGGTTCTTGAACACCATGCACTGCG 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGGCGGTTCTTGAACACCATGCACTGCG 2100
QY 2101 GGCAGCTCGGACCTTTTACTTGGTCAAGGATGCGGATGCTTCCGGTGGCGGCTGCG 2160
Db 2101 GGCAGCTCGGACCTTTTACTTGGTCAAGGATGCGGATGCTTCCGGTGGCGGCTGCG 2160
QY 2161 GGCAGACAGCGGGGAGCTTCTTCCCGGCGCGCTCTCTCTACTTGAAGGGCTCTTCG 2220
Db 2161 GGCAGACAGCGGGGAGCTTCTTCCCGGCGCGCTCTCTCTACTTGAAGGGCTCTTCG 2220
QY 2221 GCGGTCTCACTGCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGTGTC 2280
Db 2221 GCGGTCTCACTGCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTGCGAAGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACACATATG 2340
Db 2281 ACCGAGGGGTTGCGAAGCGGTGGACTTTGTATCCCGTCGAGTCTATGGAACACATATG 2340
QY 2341 CGGTCCCGGCTTCTACCGGACAACTCGTCCCTCGCGCGTACCGCAGACATTCAGGTG 2400
Db 2341 CGGTCCCGGCTTCTACCGGACAACTCGTCCCTCGCGCGTACCGCAGACATTCAGGTG 2400
QY 2401 GCCCATCTACAGCCCTTACTGTAGCGCAAGAGCACTAAGGTGCGGCTGGGTATGCA 2460
Db 2401 GCCCATCTACAGCCCTTACTGTAGCGCAAGAGCACTAAGGTGCGGCTGGGTATGCA 2460
QY 2461 GCCAAGGATTAAGGTGCTTCTCTGAACCCGTCGTCGCCACCCCTAGTTTCGGG 2520
Db 2461 GCCAAGGATTAAGGTGCTTCTCTGAACCCGTCGTCGCCACCCCTAGTTTCGGG 2520

Qy	2521	GCGTATATGCTAAAGGCACATGTATCGACCCTTAACATCAGAACCGGGTTAAGGACCATC	2580
Db	2521	GCGTATATGCTAAAGGCACATGTATCGACCCTTAACATCAGAACCGGGTTAAGGACCATC	2580
Qy	2581	ACAACGGGTGCCCCCATCACGTACTCAACTATGGCAAAGTTTTCTTGCCGACCGGTGGTC	2640
Db	2581	ACAACGGGTGCCCCCATCACGTACTCAACTATGGCAAAGTTTTCTTGCCGACCGGTGGTC	2640
Qy	2641	TCTGGGGGGCGCTATGACATCATTAATAATGATGAGTGCCCACTCAACTCGACCACT	2700
Db	2641	TCTGGGGGGCGCTATGACATCATTAATAATGATGAGTGCCCACTCAACTCGACCACT	2700
Qy	2701	ATCCTGGGCATCGGCACAGCTCTTGGAACAAAGCGAGACGGCTGGAGCGGACATCTGTCGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGCTCTTGGAACAAAGCGAGACGGCTGGAGCGGACATCTGTCGTG	2760
Qy	2761	CTCGCACCGGTACGCTTCGGGATTCGGTCACTGCGGACATCACTCAACATCGAGGAGGTG	2820
Db	2761	CTCGCACCGGTACGCTTCGGGATTCGGTCACTGCGGACATCACTCAACATCGAGGAGGTG	2820
Qy	2821	GCTCTGTCCAGCACTGGAGAATCCCCTTTTATGGCAAAGCCATCCCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGGAGAATCCCCTTTTATGGCAAAGCCATCCCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGACCTCAITTTCTGCOATTCCAAGAAAGAAATGTGATGAGCTCGCGCG	2940
Db	2881	AAGGGGGGAGGACCTCAITTTCTGCOATTCCAAGAAAGAAATGTGATGAGCTCGCGCG	2940
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACCGGGGCTTGATGATCCGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACCGGGGCTTGATGATCCGTC	3000
Qy	3001	ATACCAACTAGCGGAGACGTCTATGCTGAGCAACGGACGCTCTAAATGACGGGCTTTACC	3060
Db	3001	ATACCAACTAGCGGAGACGTCTATGCTGAGCAACGGACGCTCTAAATGACGGGCTTTACC	3060
Qy	3061	GGCGATTTCCGACTCAGTGTATCGACTGCAATATGTCACCCAGACAGTGCATTCAGC	3120
Db	3061	GGCGATTTCCGACTCAGTGTATCGACTGCAATATGTCACCCAGACAGTGCATTCAGC	3120
Qy	3121	CTGGACCGGACCTTACCATTTGAGACGACGCGTGCACAGACGCGGTGTCAGCTCG	3180
Db	3121	CTGGACCGGACCTTACCATTTGAGACGACGCGTGCACAGACGCGGTGTCAGCTCG	3180
Qy	3181	CAGCGGAGGACGAGTGTGAGGCGAGGATGGGCAITTTACAGGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGGAGGACGAGTGTGAGGCGAGGATGGGCAITTTACAGGTTTGTGACTCCAGGA	3240
Qy	3241	GAACGGCCCTCGGSCATGTTTCAATCTCGTTCGTGAGTGTATGACGCGGGCTGT	3300
Db	3241	GAACGGCCCTCGGSCATGTTTCAATCTCGTTCGTGAGTGTATGACGCGGGCTGT	3300
Qy	3301	GCTTGTGACGAGCTACGCGCGCGGAGACCTCAGTTAGTTGGGGCTTACCTTAACACA	3360
Db	3301	GCTTGTGACGAGCTACGCGCGCGGAGACCTCAGTTAGTTGGGGCTTACCTTAACACA	3360
Qy	3361	CCAGGGTTGCCGCTCTGCAAGGACCATCTGAGTTCTGGAGAGCGTCTTTTACAGGCCCTC	3420
Db	3361	CCAGGGTTGCCGCTCTGCAAGGACCATCTGAGTTCTGGAGAGCGTCTTTTACAGGCCCTC	3420
Qy	3421	ACCCACATAGACGCCATTTCTTGCCACACTAAGCAGCAGGACACACTTCCCTTAC	3480
Db	3421	ACCCACATAGACGCCATTTCTTGCCACACTAAGCAGCAGGACACACTTCCCTTAC	3480
Qy	3481	CTGTTAGCATACAGGCTACCGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC	3540
Db	3481	CTGTTAGCATACAGGCTACCGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC	3540
Qy	3541	CAAAATGTGGAAGTGTCTATACGGCTAAGGCTTACGCTGACAGGGCCAAAGCCCTGCTG	3600
Db	3541	CAAAATGTGGAAGTGTCTATACGGCTAAGGCTTACGCTGACAGGGCCAAAGCCCTGCTG	3600
Qy	3601	TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATAAACAAATACATC	3660

Db	7981	AGATCAAGTACT	7992	
RESULT 5				
AA	47281			
ID	AAU47281	standard; DNA; 7992 BP.		
XX	AA			
XX	AC			
XX	AA47281;			
XX				
DT	30-AUG-2002	(first entry)		
XX				
DE	Hepatitis C virus sub-genomic replicon recombinant clone HCVR24.			
XX				
XX	Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;			
KW	virucide; hepatotropic; gene therapy; anti-viral; gene; ds.			
KW				
XX				
OS	Hepatitis C virus.			
XX				
PN	WO200238793-A2.			
XX				
XX	16-MAY-2002.			
PF				
XX	02-NOV-2001; 2001WO-US046350.			
XX				
PR	07-NOV-2000; 2000US-0245866P.			
XX				
PA	(ANAD-) ANADYS PHARM INC.			
XX				
XX	Bichko V;			
XX				
XX	WPI; 2002-490082/52.			
XX				
XX	Novel nucleic acid encoding replication competent recombinant hepatitis C			
PT	virus genome useful for screening anti-hepatitis C virus therapeutics and			
PT	for vaccine development.			
XX				
PS	Claim 11; Page 70-75; 85pp; English.			
XX				
CC	The present invention provides protein and coding sequences from			
CC	Hepatitis C virus (HCV), comprising all or part of the HCV genome and			
CC	able to replicate efficiently when transfected into a susceptible cell			
CC	line without reducing the growth rate of the cell line by more than 10			
CC	fold. The sequences are useful for screening for anti-HCV therapeutics,			
CC	for detecting antibodies to HCV in a biological sample such as blood,			
CC	serum, plasma, blood cells, lymphocytes, or liver cells from a subject,			
CC	for deriving authentic HCV components such as replication-complement non-			
CC	infectious, replication-defective infection-component, and replication-			
CC	defective non-infectious HCV, in gene therapy or gene vaccination			
CC	targeted to hepatic tissue for treating an animal infected or susceptible			
CC	to HCV infection and for studying HCV infection and propagation. The			
CC	present sequence is a clone of a fragment of the HCV genome designated			
CC	HCVR24			
XX				
SS	Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;			
Query Match	100.0%;	Score 7990.4;	DB 6;	Length 7992;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 7991;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;
QY	1	GCCAGCCCCGATGCGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60	
Db	1	GCCAGCCCCGATGCGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60	
QY	61	TCTTCACGCAAAAGCGCTTACGCAATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120	
Db	61	TCTTCACGCAAAAGCGCTTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120	
QY	121	CCCCCTCCCGGAGGCCATAGTGGTCTCGGAACCGGTGAGTACACCGGAATTCGCGAG	180	
Db	121	CCCCCTCCCGGAGGCCATAGTGGTCTCGGAGACCGGTGAGTACACCGGAATTCGCGAG	180	
QY	181	GACGACCGGGTCTCTTCTTGGATCAACCGCTCAATGCCTGGAGATTGGGGGTGCCCCC	240	

Db 181 GACGACGGGTCTTCTTCTGATCAACCCGCTCAATGCTTGGAGATTGGGCGTGCCTCC 240
QY 241 GCGAGACTGTACGCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCTGTATAGG 300
Db 241 GCGAGACTGTACGCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCTGTATAGG 300
QY 301 GTGCTTGGAGTGCCTCCGCGGAGTCTCGTAGACGCTGACATGAGCAGAACTCTAAAC 360
Db 301 GTGCTTGGAGTGCCTCCGCGGAGTCTCGTAGACGCTGACATGAGCAGAACTCTAAAC 360
QY 361 CTCAAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTCGAGCAGGTTCTC 420
Db 361 CTCAAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTCGAGCAGGTTCTC 420
QY 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
Db 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
QY 481 CTGATGCCCGCTGTTCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540
Db 481 CTGATGCCCGCTGTTCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540
QY 541 ACTGTCCGCTGCCCTGATGAATGACGAGCAGGAGCGCGGCTATCGTGGCTGGCCA 600
Db 541 ACTGTCCGCTGCCCTGATGAATGACGAGCAGGAGCGCGGCTATCGTGGCTGGCCA 600
QY 601 CGAGCGGCGTTCCTTGGCGAGCTGTGCGAGCTTGTCACTGAAGCGGAAGGACTGCG 660
Db 601 CGAGCGGCGTTCCTTGGCGAGCTGTGCGAGCTTGTCACTGAAGCGGAAGGACTGCG 660
QY 661 TGCTATTGGCGAGTGTCCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 720
Db 661 TGCTATTGGCGAGTGTCCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 720
QY 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGATACGCTTGTGATCGCTGCTGCCGAGA 780
Db 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGATACGCTTGTGATCGCTGCTGCCGAGA 780
QY 781 CATTGCGACCAAGCGAACAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCGGCTC 840
Db 781 CATTGCGACCAAGCGAANAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCGGCTC 840
QY 841 TTGTCGATCAGGATGATCGACCAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCG 900
Db 841 TTGTCGATCAGGATGATCGACCAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCG 900
QY 901 CAGGCTCAAGGCGCGCATGCCGCGGAGGATCTCGTGTGACCCATGCGGATGCTCCT 960
Db 901 CAGGCTCAAGGCGCGCATGCCGCGGAGGATCTCGTGTGACCCATGCGGATGCTCCT 960
QY 961 GCTTGGCGAATCATGCTGGTGGAAAAATGGCCGCTTTCTGGAATTCATCGACTGTGGCCGGC 1020
Db 961 GCTTGGCGAATCATGCTGGTGGAAAAATGGCCGCTTTCTGGAATTCATCGACTGTGGCCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGTGATATGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGTGATATGCTGAAGAGC 1080
QY 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGATTCGCGCTCCCGATTCGC 1140
Db 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGATTCGCGCTCCCGATTCGC 1140
QY 1141 AGCGCATCGCTTCTATTCGCTTCTTGGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGCATCGCTTCTATTCGCTTCTTGGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
QY 1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATGTTTATTTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATGTTTATTTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTTGGCCCTCTCTTCTTGTGACGAGCATTCCT 1380
Db 1321 CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTTGGCCCTCTCTTCTTGTGACGAGCATTCCT 1380
QY 1381 AGGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTGCTGGAAGAGCA 1440
Db 1381 AGGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTGCTGGAAGAGCA 1440
QY 1441 GTTCTCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCCCTTTGCAAGGAGCGG 1500
Db 1441 GTTCTCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCCCTTTGCAAGGAGCGG 1500
QY 1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1560
Db 1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1560
QY 1561 GCAAAAGGCGGCACACCCAGTGCCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1620
Db 1561 GCAAAAGGCGGCACACCCAGTGCCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1620
QY 1621 TGCTCTCTCTCAAGCTATTCAACAAAGGCGCTGAGGATGCCAGAGGTACCCATGCT 1680
Db 1621 TGCTCTCTCTCAAGCTATTCAACAAAGGCGCTGAGGATGCCAGAGGTACCCATGCT 1680
QY 1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTGTTTAGTCGAGGTTAAAA 1740
Db 1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTGTTTAGTCGAGGTTAAAA 1740
QY 1741 AACGCTTAGGCGGCGGCAACCCAGTGCCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1800
Db 1741 AACGCTTAGGCGGCGGCAACCCAGTGCCTCTCGGCCAAAGGCAAGCCAGTGTATAGATACACCT 1800
QY 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGGCGCTACTTGGCTGATCATCACT 1860
Db 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGGCGCTACTTGGCTGATCATCACT 1860
QY 1861 AGCTCTCAGGCGGAGCAGGAACAGGTCTGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
Db 1861 AGCTCTCAGGCGGAGCAGGAACAGGTCTGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
QY 1921 ACACAACTTTTCTCGCGACTGCGTCAATGGGCTGTGTTGGAATGCTATCATGTTGCC 1980
Db 1921 ACACAACTTTTCTCGCGACTGCGTCAATGGGCTGTGTTGGAATGCTATCATGTTGCC 1980
QY 1981 GGCTCAAAAGACCTTGGCGGCGGCAACAGGCGGCGCTTCTTGGACATGACCAATGTGGAC 2040
Db 1981 GGCTCAAAAGACCTTGGCGGCGGCAACAGGCGGCGCTTCTTGGACATGACCAATGTGGAC 2040
QY 2041 CAGGACTCTGCTGGCTGGCAAGCGGCGGCGGCTTCTTGGACATGACCAATGTGGAC 2100
Db 2041 CAGGACTCTGCTGGCTGGCAAGCGGCGGCGGCTTCTTGGACATGACCAATGTGGAC 2100
QY 2101 GGCAGCTCTGAGCTTACTTGTGTCAGAGGATGCCGATGCTATCCGTCGCGCGCGG 2160
Db 2101 GGCAGCTCTGAGCTTACTTGTGTCAGAGGATGCCGATGCTATCCGTCGCGCGCGG 2160
QY 2161 GGCAGCAGCAGGGGAGCTTACTCTCCCGGCGGCGCTCTCTTGAAGGCTCTTCG 2220
Db 2161 GGCAGCAGCAGGGGAGCTTACTCTCCCGGCGGCGCTCTCTTGAAGGCTCTTCG 2220
QY 2221 GGCAGTCTGCTCTGCGGCGGCGCTGCTGCGGCGGCTTCTTGGGCTGCGGCTGTC 2280
Db 2221 GGCAGTCTGCTCTGCGGCGGCGCTGCTGCGGCGGCTTCTTGGGCTGCGGCTGTC 2280
QY 2281 ACCGAGGGGTTGCGAAGGCGGCTGAGTGTGACCGCTGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGGTTGCGAAGGCGGCTGAGTGTGACCGCTGAGTCTATGGAACCACTATG 2340
QY 2341 CCGTCCCCTGCTTTCACGCAACCTCGTCCCCTCGGCGGCTACCGCAGACATTCAGGTG 2400
Db 2341 CCGTCCCCTGCTTTCACGCAACCTCGTCCCCTCGGCGGCTACCGCAGACATTCAGGTG 2400

Db 181 GACGACGGGTCTTCTTCTGATCAACCCGCTCAATGCTTGGAGATTGGGCGTGCCTCC 240
QY 241 GCGAGACTGTACGCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCTGTATAGG 300
Db 241 GCGAGACTGTACGCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCTGTATAGG 300
QY 301 GTGCTTGGAGTGCCTCCGCGGAGTCTCGTAGACGCTGACATGAGCAGAACTCTAAAC 360
Db 301 GTGCTTGGAGTGCCTCCGCGGAGTCTCGTAGACGCTGACATGAGCAGAACTCTAAAC 360
QY 361 CTCAAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTCGAGCAGGTTCTC 420
Db 361 CTCAAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTCGAGCAGGTTCTC 420
QY 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
Db 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGCT 480
QY 481 CTGATGCCCGCTGTTCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540
Db 481 CTGATGCCCGCTGTTCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540
QY 541 ACTGTCCGCTGCCCTGATGAATGACGAGCAGGAGCGCGGCTATCGTGGCTGGCCA 600
Db 541 ACTGTCCGCTGCCCTGATGAATGACGAGCAGGAGCGCGGCTATCGTGGCTGGCCA 600
QY 601 CGAGCGGCGTTCCTTGGCGAGCTGTGCGAGCTTGTCACTGAAGCGGAAGGACTGCG 660
Db 601 CGAGCGGCGTTCCTTGGCGAGCTGTGCGAGCTTGTCACTGAAGCGGAAGGACTGCG 660
QY 661 TGCTATTGGCGAGTGTCCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 720
Db 661 TGCTATTGGCGAGTGTCCGCGCTGTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 720
QY 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGATACGCTTGTGATCGCTGCTGCCGAGA 780
Db 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGATACGCTTGTGATCGCTGCTGCCGAGA 780
QY 781 CATTGCGACCAAGCGAACAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCGGCTC 840
Db 781 CATTGCGACCAAGCGAANAATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCGGCTC 840
QY 841 TTGTCGATCAGGATGATCGACCAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCG 900
Db 841 TTGTCGATCAGGATGATCGACCAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCG 900
QY 901 CAGGCTCAAGGCGCGCATGCCGCGGAGGATCTCGTGTGACCCATGCGGATGCTCCT 960
Db 901 CAGGCTCAAGGCGCGCATGCCGCGGAGGATCTCGTGTGACCCATGCGGATGCTCCT 960
QY 961 GCTTGGCGAATCATGCTGGTGGAAAAATGGCCGCTTTCTGGAATTCATCGACTGTGGCCGGC 1020
Db 961 GCTTGGCGAATCATGCTGGTGGAAAAATGGCCGCTTTCTGGAATTCATCGACTGTGGCCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGTGATATGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGTGATATGCTGAAGAGC 1080
QY 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGATTCGCGCTCCCGATTCGC 1140
Db 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGATTCGCGCTCCCGATTCGC 1140
QY 1141 AGCGCATCGCTTCTATTCGCTTCTTGGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGCATCGCTTCTATTCGCTTCTTGGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
QY 1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATGTTTATTTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATGTTTATTTTCCACCATATG 1320

QY	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA	2460
DB	2401	GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA	2460
QY	2461	GCCCAAGGGTAAAGGTGCTTCTCTGTAACCCGTCGTCGCGCCGACCCCTAGTTTCGGG	2520
DB	2461	GCCCAAGGGTAAAGGTGCTTCTCTGTAACCCGTCGTCGCGCCGACCCCTAGTTTCGGG	2520
QY	2521	GCGTATATGCTAAAGGCACATGGTATCGACCTAAACATCAGAACCGGGTAGAGCAATC	2580
DB	2521	GCGTATATGCTAAAGGCACATGGTATCGACCTAAACATCAGAACCGGGTAGAGCAATC	2580
QY	2581	ACACGGGTGCCCCCATCAGCTACTCCACTATGGCAAGTTTCTGCCGACCGTGGTTGC	2640
DB	2581	ACACGGGTGCCCCCATCAGCTACTCCACTATGGCAAGTTTCTGCCGACCGTGGTTGC	2640
QY	2641	TCGTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700
DB	2641	TCGTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700
QY	2701	ATCCTGGGCATCGGCACAGTCTCGACCAAGCGGAGACGGCTGGAGGCGACTGTCGTG	2760
DB	2701	ATCCTGGGCATCGGCACAGTCTCGACCAAGCGGAGACGGCTGGAGGCGACTGTCGTG	2760
QY	2761	CTCGCCACCGCTACGCCCTCGGGATCGGTCAACGTCGACATCCMAACATCGAGGAGGTG	2820
DB	2761	CTCGCCACCGCTACGCCCTCGGGATCGGTCAACGTCGACATCCMAACATCGAGGAGGTG	2820
QY	2821	GCTCTGTCAGACCTGAGAGAAATCCCCCTTTATGGCAAGGCCATCCCCATCGAGCAATC	2880
DB	2821	GCTCTGTCAGACCTGAGAGAAATCCCCCTTTATGGCAAGGCCATCCCCATCGAGCAATC	2880
QY	2881	AAGGGGGGGAGGCACTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG	2940
DB	2881	AAGGGGGGGAGGCACTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG	2940
QY	2941	AAGCTGTCGGGCTCGGACTCAATCTGTAGCATATTACCGGGGCTTTGATGTATCGGTC	3000
DB	2941	AAGCTGTCGGGCTCGGACTCAATCTGTAGCATATTACCGGGGCTTTGATGTATCGGTC	3000
QY	3001	ATACCAACTAGCGGAGAGCTCATTTCTGTAGCAACGGAGCGCTCTAATGACGGGCTTTACC	3060
DB	3001	ATACCAACTAGCGGAGAGCTCATTTCTGTAGCAACGGAGCGCTCTAATGACGGGCTTTACC	3060
QY	3061	GCGGATTTGCACTAGTGAATGACCTGCAATATCATGTGTCAACCGACAGTGCAGCTCAGC	3120
DB	3061	GCGGATTTGCACTAGTGAATGACCTGCAATATCATGTGTCAACCGACAGTGCAGCTCAGC	3120
QY	3121	CTGGACCCGACCTTACCACTTGGAGCAGCAGCGTGGCCACAGACGGGTGTCAAGCTCG	3180
DB	3121	CTGGACCCGACCTTACCACTTGGAGCAGCAGCGTGGCCACAGACGGGTGTCAAGCTCG	3180
QY	3181	CAGCGGAGGAGGAGGACTGCTAGGGGACGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240
DB	3181	CAGCGGAGGAGGAGGACTGCTAGGGGACGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240
QY	3241	GAAACGGCCCTCGGGCATGTTGATTTCTGCGAGTGTATGAGTGTGCTGATCAGCGGCTGT	3300
DB	3241	GAAACGGCCCTCGGGCATGTTGATTTCTGCGAGTGTATGAGTGTGCTGATCAGCGGCTGT	3300
QY	3301	GCTTGTGTAGAGCTCAGCCCGCGGACCTCAGTTAGTTGCGGCTTACCTAAACACA	3360
DB	3301	GCTTGTGTAGAGCTCAGCCCGCGGACCTCAGTTAGTTGCGGCTTACCTAAACACA	3360
QY	3361	CCAGGGTTGCCGCTCGCAGGACCATCTGGAGTCTCTGGAGTGTCTTTACAGGCTC	3420
DB	3361	CCAGGGTTGCCGCTCGCAGGACCATCTGGAGTCTCTGGAGTGTCTTTACAGGCTC	3420
QY	3421	ACCCACATAGACGCTTCTGCTCCAGACTAAGCAGGACGAGACAACTTCCCTTAC	3480
DB	3421	ACCCACATAGACGCTTCTGCTCCAGACTAAGCAGGACGAGACAACTTCCCTTAC	3480
QY	3481	CTGTAGCATACAGGCTACGCTGTGCGCCAGGGCTCAGGCTCCACTTCATCTCGTGGAC	3540
DB	3481	CTGTAGCATACAGGCTACGCTGTGCGCCAGGGCTCAGGCTCCACTTCATCTCGTGGAC	3540
QY	3541	CAAAATGTGGAAAGTGTCTCATACGGCTAAAGCTTAAGCTTACGCTGCAAGGGCCAAAGCCCTGCTG	3600
DB	3541	CAAAATGTGGAAAGTGTCTCATACGGCTAAAGCTTAAGCTTACGCTGCAAGGGCCAAAGCCCTGCTG	3600
QY	3601	TATAGCTGGGAGCGGTTCAAAAACGAGCTTACTACCAACACACACCCCAATAACAAATACATC	3660
DB	3601	TATAGCTGGGAGCGGTTCAAAAACGAGCTTACTACCAACACACACCCCAATAACAAATACATC	3660
QY	3661	ATGGCATCATGTCGCTGACCTGAGGTCGTCACAGCACTGCGGTGTGTGTAGGCGGA	3720
DB	3661	ATGGCATCATGTCGCTGACCTGAGGTCGTCACAGCACTGCGGTGTGTGTAGGCGGA	3720
QY	3721	GTCTTAGCAGCTCTGCGCGCGTATTGCTGCTGACAAACAGGACGCTGTGTATGTGGCAGG	3780
DB	3721	GTCTTAGCAGCTCTGCGCGCGTATTGCTGCTGACAAACAGGACGCTGTGTATGTGGCAGG	3780
QY	3781	ATCATCTTGTCCGAAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
DB	3781	ATCATCTTGTCCGAAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
QY	3841	GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAAACAGGGAATGCACTCGCC	3900
DB	3841	GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAAACAGGGAATGCACTCGCC	3900
QY	3901	GAAACAATTCAAAACAGAAAGCAATCGGGTTGCTCTCAACACAGCCACCAAGCAAGCGGAGCT	3960
DB	3901	GAAACAATTCAAAACAGAAAGCAATCGGGTTGCTCTCAACACAGCCACCAAGCAAGCGGAGCT	3960
QY	3961	GCTGCTCCGCTGTGGAAATCCAAAGTGGCGACCTCGAAAGCTTTCTGGGCGAAGCATATG	4020
DB	3961	GCTGCTCCGCTGTGGAAATCCAAAGTGGCGACCTCGAAAGCTTTCTGGGCGAAGCATATG	4020
QY	4021	TGGAATTTTATCAGCGGAGTACAAATATTAGCAGGCTGTGCTCACTGCTGCTGGCAACCCC	4080
DB	4021	TGGAATTTTATCAGCGGAGTACAAATATTAGCAGGCTGTGCTCACTGCTGCTGGCAACCCC	4080
QY	4081	GCGATAGCATACATGATGGGATTCACAGCTCTATACAGCCCGCTCACCAACCAACAT	4140
DB	4081	GCGATAGCATACATGATGGGATTCACAGCTCTATACAGCCCGCTCACCAACCAACAT	4140
QY	4141	ACCTCTCTGTTTACATCTCTGGGGGATGGGTGCGCGCCCAACTTGTCTCTCCAGGCGCT	4200
DB	4141	ACCTCTCTGTTTACATCTCTGGGGGATGGGTGCGCGCCCAACTTGTCTCTCCAGGCGCT	4200
QY	4201	GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTGTGGCAGCATAGGCTTCGG	4260
DB	4201	GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTGTGGCAGCATAGGCTTCGG	4260
QY	4261	AAGTGTCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGGCC	4320

QY	7861	TTTTTCTCCTTTTTCCTTTCTTTCTTTGCGGTCCATCTTAGCCCTAGTCACGGC	7920
Dd	7861	TTTTTTCCTCTTTTTCCTTTCTTTCTTTGCGGTCCATCTTAGCCCTAGTCACGGC	7920
QY	7921	TAGCTGTGAAGGTCCTGTAGCGCGCTTGACTGCAGAGAGTCTGATACTGGCCTCTCTGC	7980
Dd	7921	TAGCTGTGAAGGTCCTGTAGCGCGCTTGACTGCAGAGAGTCTGATACTGGCCTCTCTGC	7980
QY	7981	AGATCAAGTACT 7992	
Dd	7981	AGATCAAGTACT 7992	
 RESULT 6 ABK91448 standard; DNA; 10690 BP.			
XX	AC	ABK91448;	
XX	DT	15-NOV-2002 (first entry)	
XX	DE	Hepatitis C virus vector construct pHCVNeo.17ml5.	
XX	KW	HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;	
KW	KW	hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;	
KW	KW	internal ribosome entry site; IRES; NS5A; HCV replication; mutant.	
XX	OS	Hepatitis C virus.	
OS	OS	Encephalomyocarditis virus.	
OS	OS	Escherichia coli.	
OS	OS	Enterobacteria phage T7.	
OS	OS	Synthetic.	
XX	Key	Location/Qualifiers	
FH	FT	5'UTR	1..341
FT	FT		/*tag= a
FT	FT	CDS	342..1181
FT	FT		/*tag= b
FT	FT		/product= "Core-neo fusion protein"
FT	FT	misc_signal	1190..1800
FT	FT		/*tag= c
FT	FT		/label= IRES
FT	FT		/note= "Internal ribosome entry site from BCMV"
FT	FT		1801..7758
FT	FT		/*tag= d
FT	FT		/product= "Polyprotein"
FT	FT		/note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT	FT	mutation	replace(5320,G)
FT	FT		/*tag= e
FT	FT	3'UTR	7759..7991
FT	FT		/*tag= f
FT	FT	misc_feature	7992..10690
FT	FT		/*tag= g
FT	FT		/note= "Plasmid derived sequences"
XX	PN	WO200259321-A2.	
XX	PD	01-AUG-2002.	
XX	PF	16-JAN-2002; 2002MO-EP000526.	
XX	PR	23-JAN-2001; 2001US-0263479P.	
XX	PA	(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.	
XX	PI	De Francesco R, Migliaccio G, Paonessa G;	
XX	WI	WPI; 2002-599793/64.	
XX	DR	New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV	
PT	PT	NS5 encoding region, or encephalomyocarditis virus (EMCV) internal	
PT	PT	ribosome entry site (IRES) region, useful in studying HCV replication at	
PT	PT	expression.	

xx PS Claim 16; Page; 69pp; English.

xx CC The invention relates to nucleic acid molecules comprising altered HCV

xx CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)

xx CC internal ribosome entry site (IRES) region coding for one or more NS3,

xx CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations

xx CC are detailed in the specification. Also included are (1) an expression

xx CC vector comprising a nucleotide sequence coding for the altered nucleic

xx CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a

xx CC recombinant cell human hepatoma cell comprising the altered nucleic acids

xx CC ; (3) a recombinant cell produced by introducing into a human hepatoma

xx CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)

xx CC an HCV replicon enhanced cells made in the method; and (6) measuring the

xx CC ability of a compound to affect HCV activity. The HCV replicons and HCV

xx CC replicon enhanced cells are useful in studying HCV replication and

xx CC expression, and HCV and host cell interactions, producing HCV RNA and

xx CC proteins, and providing a system for measuring the ability of a compound

xx CC to modulate one or more HCV activities e.g. to discover drugs which may

xx CC treat HCV mediated diseases such as liver failure, cirrhosis and

xx CC hepatocellular carcinoma. The present sequence is an HCV based vector

xx CC PHCVNeo.17 mutant of the invention. Note: The present sequence is not

xx CC shown in the specification but was created by the indexer using the HCV

xx CC vector sequence appearing as ABK91412 and the information in Claim 16

SQ Sequence 10690 BP; 2335 A; 3045 C; 2907 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCACGCCCGATTTGGGCGGACACTCACCATAGATCACTCCCTGTGAGGAATCTACTG 60

DB 1 GCCACGCCCGATTTGGGCGGACACTCACCATAGATCACTCCCTGTGAGGAATCTACTG 60

QY 61 TCTTCACGACAGAAAGCGTCTAGCCATGCGTGTAGTATGAGTGTCTGAGGCTCCAGGAC 120

DB 61 TCTTCACGACAGAAAGCGTCTAGCCATGCGTGTAGTATGAGTGTCTGAGGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCGCAG 180

DB 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCGCAG 180

QY 181 GACGACCGGTTCCTTCTTGATCAACCCCGCTCAATGCTCGAGATTGGCGGTGCCCC 240

DB 181 GACGACCGGTTCCTTCTTGATCAACCCCGCTCAATGCTCGAGATTGGCGGTGCCCC 240

QY 241 GCGAGACTGCTAGCCGAGTAGTGTGCGTCCGAAAGCCCTTGTGACTCCCTGATAGG 300

DB 241 GCGAGACTGCTAGCCGAGTAGTGTGCGTCCGAAAGCCCTTGTGACTCCCTGATAGG 300

QY 301 GTGCTTCGAGTGCCCGGAGGTCTCGTAGCCGTGCACCATGAGCAGCAATCCTAAAC 360

DB 301 GTGCTTCGAGTGCCCGGAGGTCTCGTAGCCGTGCACCATGAGCAGCAATCCTAAAC 360

QY 361 CTCAAGAAACCAAGGGCGGCCATGATGAAAGATGAGTTCACGCGAGTTC 420

DB 361 CTCAAGAAACCAAGGGCGGCCATGATGAAAGATGAGTTCACGCGAGTTC 420

QY 421 CGGCGCTTGGGTGGAGAGCTATTGCGCTATGACTGGGACACACAGCAATCGGTGCT 480

DB 421 CGGCGCTTGGGTGGAGAGCTATTGCGCTATGACTGGGACACACAGCAATCGGTGCT 480

QY 481 CTGATGCGCGGTGTTCCGCTGTACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540

DB 481 CTGATGCGCGGTGTTCCGCTGTACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540

QY 541 ACCTGTCCGCTGCGCTGAATGAATGAGTGAACGAGGACGCGCGCTATCGTGGCTGGCCA 600

DB 541 ACCTGTCCGCTGCGCTGAATGAATGAGTGAACGAGGACGCGCGCTATCGTGGCTGGCCA 600

QY 601 CGACGGCGGTTCCTTTCGCGAGCTGTCTCGACGTTGTACTGAAGCGGAGGACTGGC 660

DB 601 CGACGGCGGTTCCTTTCGCGAGCTGTCTCGACGTTGTCACTGAAGCGGAGGACTGGC 660

QY 661 TGTATTGGCGGAAGTGCCTGGGGCAGGATCTCTGTCTCATCTCACTTGTCTCTGGCGAGA 720

DB 661 TGTATTGGCGGAAGTGCCTGGGGCAGGATCTCTGTCTCATCTCACTTGTCTCTGGCGAGA 720

QY 721 AAGTATCCATCATGCTGTGATGCAATCGGCGGTGTCATAGCTTGTATCCGGCTACCTGCC 780

DB 721 AAGTATCCATCATGCTGTGATGCAATCGGCGGTGTCATAGCTTGTATCCGGCTACCTGCC 780

QY 781 CATTTCCACCAACGAGCAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840

DB 781 CATTTCCACCAACGAGCAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840

QY 841 TTGTGATCAGGATGATCTGACAAAGAGCATCAGGGGCTCGCGCCAGCGGACTGTTGC 900

DB 841 TTGTGATCAGGATGATCTGACAAAGAGCATCAGGGGCTCGCGCCAGCGGACTGTTGC 900

QY 901 CCAGGCTCAAGGCGGCATGCGCGAGAGATCTCGTGTGACCCATGGCGATGCCCT 960

DB 901 CCAGGCTCAAGGCGGCATGCGCGAGAGATCTCGTGTGACCCATGGCGATGCCCT 960

QY 961 GCTTTCGCAATATCATGTGGAAATGCGCGCTTTTCTCGATTCATCGATGTGGCGGC 1020

DB 961 GCTTTCGCAATATCATGTGGAAATGCGCGCTTTTCTCGATTCATCGATGTGGCGGC 1020

QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCCGTGGCTACCGCTGATATTCGTGAGAGC 1080

DB 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCCGTGGCTACCGCTGATATTCGTGAGAGC 1080

QY 1081 TTGGCGGCGAATGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG 1140

DB 1081 TTGGCGGCGAATGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG 1140

QY 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200

DB 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200

QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTACTGGC 1260

DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTACTGGC 1260

QY 1261 CGAAGCGCTTGAATTAAGCGCGGTGTGCTGTATATGTTTATTTCCACCATATTG 1320

DB 1261 CGAAGCGCTTGAATTAAGCGCGGTGTGCTGTATATGTTTATTTCCACCATATTG 1320

QY 1321 CCGTCTTTTGGCAATGTAGGCGCCGGAACCTGGCCCTGTCTTCTTGAAGCAATTCCT 1380

DB 1321 CCGTCTTTTGGCAATGTAGGCGCCGGAACCTGGCCCTGTCTTCTTGAAGCAATTCCT 1380

QY 1381 AGGGGTCTTTCCCTCTCGCAAGGAATCAAGGTCTGTTGAATGTCGTGAAGGAAGCA 1440

DB 1381 AGGGGTCTTTCCCTCTCGCAAGGAATCAAGGTCTGTTGAATGTCGTGAAGGAAGCA 1440

QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACCTGTGTAGCGACCTTTTCAGGACGCG 1500

DB 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACCTGTGTAGCGACCTTTTCAGGACGCG 1500

QY 1501 AACCCCGCCACTCGCGACAGTGCCTCTCGCGCAAAAGCAAGCAAGTATAGATACACCT 1560

DB 1501 AACCCCGCCACTCGCGACAGTGCCTCTCGCGCAAAAGCAAGCAAGTATAGATACACCT 1560

QY 1561 GCAAGCGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620

DB 1561 GCAAGCGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620

QY 1621 TGGCTCTCTCAAGCGTATTTCAAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680

DB 1621 TGGCTCTCTCAAGCGTATTTCAAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680

QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTATGTTTATGTTTGTGAGGTTAA 1740

Db	1581	ATGGGATCTGATCTCTGGGCGCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAA	1740
Qy	1741	AACGTCCTAAGGCCCGCCCGAAACACACGGGGACGTGGTTTTCTTTTGAAGAAAACACGATATAACC	1800
Db	1741	AACGTCCTAAGGCCCGCCCGAAACACACGGGGACGTGGTTTTCTTTTGAAGAAAACACGATATAACC	1800
Qy	1801	ATGGCGCTATTACGGCCTACTCCAAACAGACCGCAGAGGCTACTTGGCTGSCATCATCACT	1860
Db	1801	ATGGCGCTATTACGGCCTACTCCAAACAGACCGCAGAGGCTACTTGGCTGSCATCATCACT	1860
Qy	1861	AGCCTCACAGGCGGGACAGAAACACAGTCGAGGGGAGGTCAAATGTGCTCCACCGCA	1920
Db	1861	AGCCTCACAGGCGGGACAGAAACACAGTCGAGGGGAGGTCAAATGTGCTCCACCGCA	1920
Qy	1921	ACACAATCTTTCTGGCGACCTGCGTCAATGGCTGTGTGGACTGTCTATCATGTGTGCC	1980
Db	1921	ACACAATCTTTCTGGCGACCTGCGTCAATGGCTGTGTGGACTGTCTATCATGTGTGCC	1980
Qy	1981	GGCTCAAGACCCCTTGCCCGCCCAAAGGGCCCAATCACCCAAATGTACCAATGTGGAC	2040
Db	1981	GGCTCAAGACCCCTTGCCCGCCCAAAGGGCCCAATCACCCAAATGTACCAATGTGGAC	2040
Qy	2041	CAGGACCTCGTCGGCTGGCAAGCGCCCGGGCGGCTCTTGACACCAATGCACCTGC	2100
Db	2041	CAGGACCTCGTCGGCTGGCAAGCGCCCGGGCGGCTCTTGACACCAATGCACCTGC	2100
Qy	2101	GGCAGCTCGGACCTTTACTTTGGTTCAGAGGACATGCCCATGTCTATCCGGGTGCGCGGCGG	2160
Db	2101	GGCAGCTCGGACCTTTACTTTGGTTCAGAGGACATGCCCATGTCTATCCGGGTGCGCGGCGG	2160
Qy	2161	GGCGACAGCAGGGGGAGCTACTCTCCCGCCAGGCGCGCTCTCTACTTGAAGGGCTCTTCG	2220
Db	2161	GGCGACAGCAGGGGGAGCTACTCTCCCGCCAGGCGCGCTCTCTACTTGAAGGGCTCTTCG	2220
Qy	2221	GGCGGTCCAATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCCGGCTGCGGTGTGC	2280
Db	2221	GGCGGTCCAATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCCGGCTGCGGTGTGC	2280
Qy	2281	ACCGAGGGTTGCGAAGGCGGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
Db	2281	ACCGAGGGTTGCGAAGGCGGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
Qy	2341	CGGTCCCGGTCTTACCGACAACCTCGTCCCTCGCGCGTACCGACACATTCAGGTG	2400
Db	2341	CGGTCCCGGTCTTACCGACAACCTCGTCCCTCGCGCGTACCGACACATTCAGGTG	2400
Qy	2401	GCCCATCTACAGCCCGCTACTGGTAGCGGCAAGACACTAAGTCCGCTCGGTATGCA	2460
Db	2401	GCCCATCTACAGCCCGCTACTGGTAGCGGCAAGACACTAAGTCCGCTCGGTATGCA	2460
Qy	2461	GCCCAAGGTTAAGGTGCTTCTGCTGAACCCGTCGTCGCCCGCCACCCCTAGGTTTCGGG	2520
Db	2461	GCCCAAGGTTAAGGTGCTTCTGCTGAACCCGTCGTCGCCCGCCACCCCTAGGTTTCGGG	2520
Qy	2521	GGGTATATGCTTAAGSCACATCGTATCGACCCCTAAATCAGAAACCGGGTAAAGCACATC	2580
Db	2521	GGGTATATGCTTAAGSCACATCGTATCGACCCCTAAATCAGAAACCGGGTAAAGCACATC	2580
Qy	2581	ACACGGGTGCCCGCATCAGCTACTCCACTATGGCAAGTCTTCTCCCGACGGTGGTTCG	2640
Db	2581	ACACGGGTGCCCGCATCAGCTACTCCACTATGGCAAGTCTTCTCCCGACGGTGGTTCG	2640
Qy	2641	TCGTGGGGCGCCTATGACATCATTAATGTGATGAGTGCCACTCAACTGACGCACT	2700
Db	2641	TCGTGGGGCGCCTATGACATCATTAATGTGATGAGTGCCACTCAACTGACGCACT	2700
Qy	2701	ATCCTGGGCATCGGCACAGTCTGGACCAAGCGGACCGGTGGAGCGGACCTCGTGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGTCTGGACCAAGCGGACCGGTGGAGCGGACCTCGTGTG	2760
Qy	2761	CTCGCACCGCTAGCCTCCGGGATCGGTCAACCGTGCACATCCAAACATCTGAGAGGTG	2820
Db	2761	CTCGCACCGCTAGCCTCCGGGATCGGTCAACCGTGCACATCCAAACATCTGAGAGGTG	2820

QY	2821	GCTCTGTC	CAGCACTG	GAGAAATCCCCTTTTAT	GGCAAGCCATCCCATCAGACCATC	2880
DB	2821	GCTCTGTC	CAGCACTG	GAGAAATCCCCTTTTAT	GGCAAGCCATCCCATCAGACCATC	2880
QY	2881	AAGGGGGG	AGGCACCTCATTTTCTG	CCATTC	CAAGAGAAATGTGATGAGCTCGCCGG	2940
DB	2881	AAGGGGGG	AGGCACCTCATTTTCTG	CCATTC	CAAGAGAAATGTGATGAGCTCGCCGG	2940
QY	2941	AAGCTGTCCG	GCTCGGACCTAATCTGTAG	CAATATACCGGGGCTTCATGTATCCGTC	3000	
DB	2941	AAGCTGTCCG	GCTCGGACCTAATCTGTAG	CAATATATACCGGGGCTTCATGTATCCGTC	3000	
QY	3001	ATACCAACTAG	CGGAGAGCTCATTCG	TAGCAACGAGCGCTTAATAGCGGCTTTTACC	3060	
DB	3001	ATACCAACTAG	CGGAGAGCTCATTCG	TAGCAACGAGCGCTTAATAGCGGCTTTTACC	3060	
QY	3061	GGCGATTTT	CGACTCAGTCTGATCG	ACTGCAATCATGTGTCA	CCAGACAGCTCGACTTCAGC	3120
DB	3061	GGCGATTTT	CGACTCAGTCTGATCG	ACTGCAATCATGTGTCA	CCAGACAGCTCGACTTCAGC	3120
QY	3121	CTGGACCCG	ACCTTACCAATGAG	AGCAGCGCTGCCCAAGACGGGTGTCA	CGCTCG	3180
DB	3121	CTGGACCCG	ACCTTACCAATGAG	AGCAGCGCTGCCCAAGACGGGTGTGTCA	CGCTCG	3180
QY	3181	CAGCGCGAGG	CAGGACTCGTAGGG	CAGGATGGGCATTTACAGGTTTGTG	ATCTCCAGGA	3240
DB	3181	CAGCGCGAGG	CAGGACTCGTAGGG	CAGGATGGGCATTTACAGGTTTGTG	ATCTCCAGGA	3240
QY	3241	GAACGGCCCT	CGGCGATGTTTCG	ATTCCTCGGTTCTGTG	CGAGTGTATGACGGGGCTGT	3300
DB	3241	GAACGGCCCT	CGGCGATGTTTCG	ATTCCTCGGTTCTGTG	CGAGTGTATGACGGGGCTGT	3300
QY	3301	GCTTGTTG	TACAGCTAC	CGCCCGCAGACCTC	AGTTAGTTGCGGGCTTACCTAAACACA	3360
DB	3301	GCTTGTTG	TACAGCTAC	CGCCCGCAGACCTC	AGTTAGTTGCGGGCTTACCTAAACACA	3360
QY	3361	CGAGGTTG	CCGCTCTG	CCAGGACCATCTG	AGTTCTGGGAGAGCGTCTTTTACAGGCGCTC	3420
DB	3361	CGAGGTTG	CCGCTCTG	CCAGGACCATCTG	AGTTCTGGGAGAGCGTCTTTTACAGGCGCTC	3420
QY	3421	ACCCACATAG	ACGCCCATTTCTTGT	CCAGACTAAG	CAGGCGAGAGCAACTTCCCCTTAC	3480
DB	3421	ACCCACATAG	ACGCCCATTTCTTGT	CCAGACTAAG	CAGGCGAGAGCAACTTCCCCTTAC	3480
QY	3481	CTGTGTAG	ATACAGGCTAC	GGTGTGCGCCAGGCGT	CAGGCTCCACCTTCCATCTGTGGAC	3540
DB	3481	CTGTGTAG	ATACAGGCTAC	GGTGTGCGCCAGGCGT	CAGGCTCCACCTTCCATCTGTGGAC	3540
QY	3541	CAAAATGTG	GAAGTGTCTCATAC	GGCTAAGCGTTC	AGCTGCAAGCGCCCAACGCCCCCTGTGTG	3600
DB	3541	CAAAATGTG	GAAGTGTCTCATAC	GGCTAAGCGTTC	AGCTGCAAGCGCCCAACGCCCCCTGTGTG	3600
QY	3601	TATAGGCTGG	GAGCGGTTTCAAA	CAGGTTTACTAC	CACACCCCATACCAAAATACATC	3660
DB	3601	TATAGGCTGG	GAGCGGTTTCAAA	CAGGTTTACTAC	CACACCCCATACCAAAATACATC	3660
QY	3661	ATGGATGCA	TGTGTGGTGTG	ACTGAGCTCGT	CAGCAGCTGGTGTCTGTAGCGCGA	3720
DB	3661	ATGGATGCA	TGTGTGGTGTG	ACTGAGCTCGT	CAGCAGCTGGTGTCTGTAGCGCGA	3720
QY	3721	GTCTAGCAG	CTCTGGCGGTTAT	TGCTGACAA	CAGGCGAGCTGTCTATGTGGGCGAG	3780
DB	3721	GTCTAGCAG	CTCTGGCGGTTAT	TGCTGACAA	CAGGCGAGCTGTCTATGTGGGCGAG	3780
QY	3781	ATCATCTTT	TCGGAAAGCCG	GCATCAT	TCCCGGACAGGAGTCTTTTACCGGAGTTC	3840
DB	3781	ATCATCTTT	TCGGAAAGCCG	GCATCAT	TCCCGGACAGGAGTCTTTTACCGGAGTTC	3840
QY	3841	GATGAGATG	GAAGTGTGCGCT	TCACACCTT	CATCGAACAGGGAATGACAGCTCGCC	3900
DB	3841	GATGAGATG	GAAGTGTGCGCT	TCACACCTT	CATCGAACAGGGAATGACAGCTCGCC	3900

3901 GAACAATTCAAACAGAGGCAATCGGGTGTCTGCAAAACAGCCACCAAGCAGCGAGGCT 3960
3901 GAACAATTCAAACAGAGGCAATCGGGTGTCTGCAAAACAGCCACCAAGCAGCGAGGCT 3960
3961 GCTGCTCCCGTGTGGAAATCAAAGTGGCGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
3961 GCTGCTCCCGTGTGGAAATCAAAGTGGCGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
4021 TGGAATTTCAATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCC 4080
4021 TGGAATTTCAATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCC 4080
4081 GCGATAGCATCACTGATGCAATTTACAGCTCTATCAGCAGCCCGCTCAACCCAAACAT 4140
4081 GCGATAGCATCACTGATGCAATTTACAGCTCTATCAGCAGCCCGCTCAACCCAAACAT 4140
4141 ACCCTCTCTTTAAACATCTGGGGGATGGTGGCGGCCCACTTCTCCTCCACGCGCT 4200
4141 ACCCTCTCTTTAAACATCTGGGGGATGGTGGCGGCCCACTTCTCCTCCACGCGCT 4200
4201 GCTTCTGCTTTTCTAGGCGCGCGCATTCGCTGAGCGGCTTGTGGCAGCATAGGCCCTTGG 4260
4201 GCTTCTGCTTTTCTAGGCGCGCGCATTCGCTGAGCGGCTTGTGGCAGCATAGGCCCTTGG 4260
4261 AAGGTGCTTGTGGATATTTTGCAGGTTATGAGCAGGGTGGCAGCGCGCTCGTGGCC 4320
4261 AAGGTGCTTGTGGATATTTTGCAGGTTATGAGCAGGGTGGCAGCGCGCTCGTGGCC 4320
4321 TTTAAGGTCAAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTTCTCCTGCT 4380
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4381 ATCCTCTCCCTGGCGCCTAGTCTGGGGTGTGTCGAGCGATACTGGTGGGCAC 4440
4381 ATCCTCTCCCTGGCGCCTAGTCTGGGGTGTGTCGAGCGATACTGGTGGGCAC 4440
4441 GTGGGCCAGGGAGGGGCGTGCAGTGGATGAACCGGCTGTATAGCCTTGGTTCGGG 4500
4441 GTGGGCCAGGGAGGGGCGTGTGAGTGGATGAACCGGCTGTATAGCCTTGGTTCGGG 4500
4501 GGTAAACACGCTCTCCCGCAGCACTATGTGCTGAGAGCGAGCTGACGACGCTGCACT 4560
4501 GGTAAACACGCTCTCCCGCAGCACTATGTGCTGAGAGCGAGCTGACGACGCTGCACT 4560
4561 CAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAGAGCGAGCTGACGACGCTGCACT 4620
4561 CAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAGAGCGAGCTGACGACGCTGCACT 4620
4621 GAGGACTGCTCCAGCCATCTCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC 4680
4621 GAGGACTGCTCCAGCCATCTCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC 4680
4681 ACGGTGTGATCTGATTTCAAGACTGCTCAGTCCAGTCCAAAGCTCTGCGCGGATTCGGGGA 4740
4681 ACGGTGTGATCTGATTTCAAGACTGCTCAGTCCAGTCCAAAGCTCTGCGCGGATTCGGGGA 4740
4741 GTCCCTTCTTCTCATGTCAAACGTTGGTACAAGGAGTCTGGCGGGCGAGCGCATCATG 4800
4741 GTCCCTTCTTCTCATGTCAAACGTTGGTACAAGGAGTCTGGCGGGCGAGCGCATCATG 4800
4801 CAAACACCTGCCCATTGTGAGCAGACATCCGGAATGTGAAACCGTTCATGAGG 4860
4801 CAAACACCTGCCCATTGTGAGCAGACATCCGGAATGTGAAACCGTTCATGAGG 4860
4861 ATGTTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACTTCCCAATTAAACGGTAC 4920
4861 ATGTTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACTTCCCAATTAAACGGTAC 4920
4921 ACCAGGGCCCTGACAGCCCTCCCGCGGCCAAATTTATCTAGGCGCTGTGGCGGGTG 4980
4921 ACCAGGGCCCTGACAGCCCTCCCGCGGCCAAATTTATCTAGGCGCTGTGGCGGGTG 4980
4981 GCTGCTGAGGAGTACGTGGAGTTACGCGGTTGGGGATTTTCACTACGTGACGGGCATG 5040

4981 GCTGCTGAGGAGTACGTGGAGTTTACCGGGTGGGGATTTCCACTACGTGACGGCATG 5040
5041 ACCACTGACAAAGTACCGGCTGTGAGTTCCGGCCCCCGAATTTCTTCAAGAGTG 5100
5041 ACCACTGACAAAGTACCGGCTGTGAGTTCCGGCCCCCGAATTTCTTCAAGAGTG 5100
5101 GATGGGTTGGTGTGACAGGTTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGAGTC 5160
5101 GATGGGTTGGTGTGACAGGTTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGAGTC 5160
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5161 ACATTCCTGCTGGGCTCAATCAATACCTGTTGGTTCAGCTCCATCGAGGCCGAA 5220
5221 CCGGAGTACGAGTGTCTACTTCCATGCTCAGCGACCCCTCCACATTAAGCGGAGAGC 5280
5221 CCGGAGTACGAGTGTCTACTTCCATGCTCAGCGACCCCTCCACATTAAGCGGAGAGC 5280
5281 GCTAAGCTGAGGCTGGCCAGGGATCTCCCCCTCTCTTGGCCAGCTCATCAGTAGCCAG 5340
5281 GCTAAGCTGAGGCTGGCCAGGGATCTCCCCCTCTCTTGGCCAGCTCATCAGTAGCCAG 5340
5341 CTGCTCTGGCCTTCTTGAAGCAACATGCACTACCCGTCATGCTCCCGGACGCTGAC 5400
5341 CTGCTCTGGCCTTCTTGAAGCAACATGCACTACCCGTCATGCTCCCGGACGCTGAC 5400
5401 CTATCGAGGCCAACCTCTGTGGCGGAGAGATGGGGGAAATCACCCGCGTGGAG 5460
5401 CTATCGAGGCCAACCTCTGTGGCGGAGAGATGGGGGAAATCACCCGCGTGGAG 5460
5461 TCAGAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGAGAGATCAG 5520
5461 TCAGAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGAGAGATCAG 5520
5521 AGGAAGTATCCGTTCCGGCGAGATCTCTGGAGGTCCAGAAATTCCTTCGAGCGCATG 5580
5521 AGGAAGTATCCGTTCCGGCGAGATCTCTGGAGGTCCAGAAATTCCTTCGAGCGCATG 5580
5581 CCCATATGGGCACGCCCGGATTACAACTTCCACTGTTAGAGTCTTGGAAAGACCCGAC 5640
5581 CCCATATGGGCACGCCCGGATTACAACTTCCACTGTTAGAGTCTTGGAAAGACCCGAC 5640
5641 TAGTCTCTCAGTGTGACAGGTTGCTCTGTAAGTCTAAGTCTAAGTCTTCTGCTTGGCG 5700
5641 TAGTCTCTCAGTGTGACAGGTTGCTCTGTAAGTCTAAGTCTAAGTCTTCTGCTTGGCG 5700
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5701 CTTCAGGAGGAGGAGGAGTGTCTCTGTAAGTCTAAGTCTAAGTCTTCTGCTTGGCG 5760
5761 GAGTCTGCCCAAAAGACCTTCCGCGAGCTCCGAATCGTCCGCGCTTCAGCAGCGGCA 5820
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5821 ACGGCTCTCTTGACCAAGCCCTCCGAGCGAGCGGGATCCCGATCTCAGCGACGCTGAC 5880
5881 TCTTCCATGCCCCCTTGAAGGAGGAGCGGGGATCCCGATCTCAGCGACGCTTGG 5940
5881 TCTTCCATGCCCCCTTGAAGGAGGAGCGGGGATCCCGATCTCAGCGACGCTTGG 5940
5941 TCTACCGTAAAGCAGGAGGAGTGTGAGGAGTGTCTGCTGCTGATGCTTCAATG 6000
5941 TCTACCGTAAAGCAGGAGGAGTGTGAGGAGTGTCTGCTGCTGATGCTTCAATG 6000
6001 ACAGGCGCCTGATCACGCCATCGCTGGAGGAAACCAAGCTGCCATCAATGCACTG 6060
6001 ACAGGCGCCTGATCACGCCATCGCTGGAGGAAACCAAGCTGCCATCAATGCACTG 6060
6061 AGCAACTCTTCTGCTCCGTCACCAAACTTGTATGTATGCTTACAACTCTCGCAGCGCAAGC 6120

6061 AGCAACTTTTGTCTCCGTCACCAACAACTTGTGTCTATGCTACACATCTCGCAGCGCAAGC 6120 Db
6121 CTGGGCGAAGAAAGGTCACTTTTACAGAGCTGACAGTCTTGGAGCAGCACTACCGGAC 6180 Qy
6121 CTGGGCGAAGAAAGGTCACTTTTACAGAGCTGACAGTCTTGGAGCAGCACTACCGGAC 6180 Db
6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTTGGAG 6240 Qy
6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTTGGAG 6240 Db
6241 GAAGCTGTAGCTGACGCGCCCAATTCGGGAGATCTTAAATTTTGGCTATATGGGCAAG 6300 Qy
6241 GAAGCTGTAGCTGACGCGCCCAATTCGGGAGATCTTAAATTTTGGCTATATGGGCAAG 6300 Db
6301 GACGTCGGGAACTTATCCAGCAAGCGTAAACCAATCCGCTCCGTTGGAAGGACTTG 6360 Qy
6301 GACGTCGGGAACTTATCCAGCAAGCGTAAACCAATCCGCTCCGTTGGAAGGACTTG 6360 Db
6361 CTGGAGACACTGAGACACCAATTTGACACCACTATGCGCAAAATGAGGTTTCTGC 6420 Qy
6361 CTGGAGACACTGAGACACCAATTTGACACCACTATGCGCAAAATGAGGTTTCTGC 6420 Db
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6421 GTCCACCGAGAGAGGCGGCGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGG 6480 Db
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6481 GTTTCGTGTGTCGAGAAATTTGGCCCTTTACGATGTGTCCTCCACCTCCCTCAGGCGTG 6540 Db
6541 ATGGGCTCTTTCATACGATTTCCAACTCTCTCGGACAGCGGTCGAGTTTCTGTGTAAT 6600 Qy
6541 ATGGGCTCTTTCATACGATTTCCAACTCTCTCGGACAGCGGTCGAGTTTCTGTGTAAT 6600 Db
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6601 GCCTGGAAGCGAAGAAATGCCCCTATGCGCTTCCATATGACACCCGCTGTTTGACTCA 6660 Db
6661 ACCTGCTCACTGAGATGACATCCGTTGTTGAGAGTCAATCTACCAATGTTGACTTGCC 6720 Qy
6661 ACCTGCTCACTGAGATGACATCCGTTGTTGAGAGTCAATCTACCAATGTTGACTTGCC 6720 Db
6721 CCCGAGCGACAGGCGCAATAGTCTGCTACAGAGCGGCTTACATCGGGGCGCCCTG 6780 Qy
6721 CCCGAGCGACAGGCGCAATAGTCTGCTACAGAGCGGCTTACATCGGGGCGCCCTG 6780 Db
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6781 ACTAATTTCTAAGGCGAGAACTGCGGCTATCGCGGCTGCGCGGAGCGGCTGACTGACG 6840 Db
6841 ACCAGCTGCGGTAATACCTCTACATGTTTAAAGGCGGCTGCGCGGCTGCGAGCTGG 6900 Qy
6841 ACCAGCTGCGGTAATACCTCTACATGTTTAAAGGCGGCTGCGCGGCTGCGAGCTGG 6900 Db
6901 AAGCTCCAGGATGTCAGAGTCTGTCGAGAGCGACTTGTCTGTTATCTGTGAAGC 6960 Qy
6901 AAGCTCCAGGATGTCAGAGTCTGTCGAGAGCGACTTGTCTGTTATCTGTGAAGC 6960 Db
6961 GCGGGGACCCAGAGGACAGGCGGAGCTTACCGGCTTCAAGGAGGCTATGACTAGATAC 7020 Qy
6961 GCGGGGACCCAGAGGACAGGCGGAGCTTACCGGCTTCAAGGAGGCTATGACTAGATAC 7020 Db
7021 TCTGCCCCCTGGGACCGGCCCAACAGAAATACGACTTGGAGTTGATTAACATCATGC 7080 Qy
7021 TCTGCCCCCTGGGACCGGCCCAACAGAAATACGACTTGGAGTTGATTAACATCATGC 7080 Db
7081 TCTTCAATGTGTGCTGCGGACGATGCTGCGGCAAAAGGCTGACTATCTCACCCTG 7140 Qy
7081 TCTTCAATGTGTGCTGCGGACGATGCTGCGGCAAAAGGCTGACTATCTCACCCTG 7140 Db
7141 GACCCACCAACCCCTTGGCGGCTGCGTGGAGACAGCTGAGACACTCCAGTCAAT 7200 Qy
7141 GACCCACCAACCCCTTGGCGGCTGCGTGGAGACAGCTGAGACACTCCAGTCAAT 7200 Db

7201 TCTGCGCTAGGCAACATCATGATGCGGCCACCTTGTGCGCAAGGATGATCTGATG 7260 Qy
7201 TCTGCGCTAGGCAACATCATGATGCGGCCACCTTGTGCGCAAGGATGATCTGATG 7260 Db
7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACCTTGAAGGCTAGATGTCAG 7320 Qy
7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACCTTGAAGGCTAGATGTCAG 7320 Db
7321 ATCTACGGGCGCTGTTACTTCCATTGAGCCACTTACCTACCTCAGATCATTTCAACGACTC 7380 Qy
7321 ATCTACGGGCGCTGTTACTTCCATTGAGCCACTTACCTACCTCAGATCATTTCAACGACTC 7380 Db
7381 CATGCGCTTAGCGCATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440 Qy
7381 CATGCGCTTAGCGCATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440 Db
7441 TCATGCTCAGGAAACTTGGGCTACCGCTTGGAGTCTGGAGACATCGGGCCAGAAGT 7500 Qy
7441 TCATGCTCAGGAAACTTGGGCTACCGCTTGGAGTCTGGAGACATCGGGCCAGAAGT 7500 Db
7501 GTCCGCGCTAGGCTACTGTCCCAGGGGGAGGCTGCGACTTGTGGCAAGTACCTTCTC 7560 Qy
7501 GTCCGCGCTAGGCTACTGTCCCAGGGGGAGGCTGCGACTTGTGGCAAGTACCTTCTC 7560 Db
7561 AACTGGCGAGTAAGGACCAAGCTCAAACTCACTCCCAATCCCGCTGCGTCCAGTTGGAT 7620 Qy
7561 AACTGGCGAGTAAGGACCAAGCTCAAACTCACTCCCAATCCCGCTGCGTCCAGTTGGAT 7620 Db
7621 TTATCCAGCTGCTGTTGCTGCTTACAGCGGGGAGACATATATCACAGCTGCTCGT 7680 Qy
7621 TTATCCAGCTGCTGTTGCTGCTTACAGCGGGGAGACATATATCACAGCTGCTCGT 7680 Db
7681 GCGCGACCCGCTGTTTCACTGCTGCTTACAGCGGGGAGACATATATCACAGCTGCTCGT 7740 Qy
7681 GCGCGACCCGCTGTTTCACTGCTGCTTACAGCGGGGAGACATATATCACAGCTGCTCGT 7740 Db
7741 CTACTCCCAACCGATGAACGCGGAGCTAAACCTCCAGGCGCAATAGGCCATCTGTTT 7800 Qy
7741 CTACTCCCAACCGATGAACGCGGAGCTAAACCTCCAGGCGCAATAGGCCATCTGTTT 7800 Db
7801 TTTCCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860 Qy
7801 TTTCCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860 Db
7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920 Qy
7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920 Db
7921 TAGCTGTGAAGGCTCCGTGAGCGGCTTCCATCTTAGCCCTAGTACCGGC 7980 Qy
7921 TAGCTGTGAAGGCTCCGTGAGCGGCTTCCATCTTAGCCCTAGTACCGGC 7980 Db
7981 AGATCAAGTACT 7992 Qy
7981 AGATCAAGTACT 7992 Db

RESULT 7

ABK91435
ID - ABK91435 standard; DNA; 10690 BP.

XX ABK91435;

XX 15-NOV-2002 (first entry)

XX Hepatitis C virus vector construct pHCVNeo.17m2.

XX HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX Hepatitis C virus.

OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

XX Key Location/Qualifiers
FH 5'UTR 1. .341
FT /*tag= a
FT 342..1181
FT /*tag= b
FT /product= "Core-neo fusion protein"
FT 1190..1800
FT /*tag= c
FT /label= IRES
FT /note= "Internal ribosome entry site from EMCV"
FT 1801..7758
FT /*tag= d
FT /product= "Polyprotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT mutation replace(5243,C)
FT /*tag= e
FT 7759..7991
FT /*tag= f
FT 7992..10690
FT /*tag= g
FT /note= "Plasmid derived sequences"

XX WO200259321-A2.

XX 01-AUG-2002.

XX 16-JAN-2002; 2002WO-EP000526.

XX 23-JAN-2001; 2001US-0263479P.

XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.

XX De Francesco R, Magliaccio G, Paonessa G;

XX WPI; 2002-599793/64.

XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression.

XX Claim 16; Page; 69pp; English.

XX The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVneo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTAGT 60
DB 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTAGT 60

QY 61 TCTTACGCGAGAAGCGTCTAGCCATGGGCTTAGTATGATGTCGTGCGACCTCCAGGAC 120
DB 61 TCTTACGCGAGAAGCGTCTAGCCATGGGCTTAGTATGATGTCGTGCGACCTCCAGGAC 120

QY 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCCTGCGAATTCGCGAATTCGCCAG 180
DB 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCCTGCGAATTCGCGAATTCGCCAG 180

QY 181 GACGACCCGGGTCTTCTTTGGATCAACCCGCTCAATGCTGCGAATTCGCGAATTCGCCAG 180
DB 181 GACGACCCGGGTCTTCTTTGGATCAACCCGCTCAATGCTGCGAATTCGCGAATTCGCCAG 180

QY 241 GCGAGCTGCTAGCCGAGTGTGTTGGGTGCGAAGGCTTGTGTAATTCGCGAATTCGCCAG 300
DB 241 GCGAGCTGCTAGCCGAGTGTGTTGGGTGCGAAGGCTTGTGTAATTCGCGAATTCGCCAG 300

QY 301 GTGCTTGGAGTGTGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCTAAC 360
DB 301 GTGCTTGGAGTGTGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCTAAC 360

QY 361 CTCAAGAAAAACAAAGGCGCGCATGATGATGACATGAGTGAATGATGATGATGATGATGAT 420
DB 361 CTCAAGAAAAACAAAGGCGCGCATGATGATGACATGAGTGAATGATGATGATGATGATGAT 420

QY 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAGCAATTCGGTGTCT 480
DB 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAGCAATTCGGTGTCT 480

QY 481 CTGATGCGCGCGTGTTCGGCTGTGCGAGGCGCGCGGCTTCTTTTGTCAAGACCG 540
DB 481 CTGATGCGCGCGTGTTCGGCTGTGCGAGGCGCGCGGCTTCTTTTGTCAAGACCG 540

QY 541 ACCTGTCCGCTGCCCTCAATGAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 ACCTGTCCGCTGCCCTCAATGAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

QY 601 CGAGCGCGCTTCTTCGCGAGCTGTGCTCGACGTTGCTCAAGCGGAGGAGGAGGAGGAGG 660
DB 601 CGAGCGCGCTTCTTCGCGAGCTGTGCTCGACGTTGCTCAAGCGGAGGAGGAGGAGGAGG 660

QY 661 TGCTATTGGGCGAAGTCCGGGCGAGATCTCTGTCAATCTCACTTGTCTTCTTCTTCTTCT 720
DB 661 TGCTATTGGGCGAAGTCCGGGCGAGATCTCTGTCAATCTCACTTGTCTTCTTCTTCTTCT 720

QY 721 AAGTATCCATCATGCTGTGATGCAATCGCGGCTGCAATCGCTTGTATCGGCTACCTGCC 780
DB 721 AAGTATCCATCATGCTGTGATGCAATCGCGGCTGCAATCGCTTGTATCGGCTACCTGCC 780

QY 781 CAFTGACCAACAAAGCAACATCGCATCGAGCGAGCAGTACTCGGATGGAGCGGCTC 840
DB 781 CAFTGACCAACAAAGCAACATCGCATCGAGCGAGCAGTACTCGGATGGAGCGGCTC 840

QY 841 TTGTGATCAGATGATCTGGAGCAAGCATCAGGGGCTCGCGGCGAGCGGAGCTGTTCG 900
DB 841 TTGTGATCAGATGATCTGGAGCAAGCATCAGGGGCTCGCGGCGAGCGGAGCTGTTCG 900

QY 901 CCAGGCTCAAGCGCGCATGCCCGAGCGAGGATCTGCTGTGACCCATGCGGAGCTTCT 960
DB 901 CCAGGCTCAAGCGCGCATGCCCGAGCGAGGATCTGCTGTGACCCATGCGGAGCTTCT 960

QY 961 GCTTCCGAATATCATGTGGAAATGCGCGCTTTTCTGGATTCATCGACTGTGCGCGGC 1020
DB 961 GCTTCCGAATATCATGTGGAAATGCGCGCTTTTCTGGATTCATCGACTGTGCGCGGC 1020

QY 1021 TGGGTGTGGGAGCGGCTATCAGGACATAGCGTTGGCTACCGCTGATATTCTGAAGAGC 1080

D _b	1021	TTGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATGCTGAAGAGC	1080
Q _y	1081	TTGGCGGCAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCGCTCCGATTCCG	1140
D _b	1081	TTGGCGGCAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCGCTCCGATTCCG	1140
Q _y	1141	AGCGCATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTTGAGTATTTAAACAGACCAACG	1200
D _b	1141	AGCGCATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTTGAGTATTTAAACAGACCAACG	1200
Q _y	1201	GTTCCTCTAGCGGGATCAATTCGCGCCTCTCCCTCCCGCCCCCTAACGTTACTGCG	1260
D _b	1201	GTTCCTCTAGCGGGATCAATTCGCGCCTCTCCCTCCCGCCCCCTAACGTTACTGCG	1260
Q _y	1261	CGAAGCGCTTGGAAATAGCGCGGTGTGGTGTCTATATGTATTTTCCACCATATTG	1320
D _b	1261	CGAAGCGCTTGGAAATAGCGCGGTGTGGTGTCTATATGTATTTTCCACCATATTG	1320
Q _y	1321	CGGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTCTCTCTTGACGACATTCT	1380
D _b	1321	CGGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTCTCTCTTGACGACATTCT	1380
Q _y	1381	AGGGGTCTTTCCCTCTCGCCCAAGGAATCAAGGTCGTGTGAATGTCTGTAAGGAGCA	1440
D _b	1381	AGGGGTCTTTCCCTCTCGCCCAAGGAATCAAGGTCGTGTGAATGTCTGTAAGGAGCA	1440
Q _y	1441	GTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTGAGGACGCG	1500
D _b	1441	GTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTGAGGACGCG	1500
Q _y	1501	AACCCCCACCTGCGCAGCAGGTGCTCTGCGGCCAAAGACCACTGTATAGATACACCT	1560
D _b	1501	AACCCCCACCTGCGCAGCAGGTGCTCTGCGGCCAAAGACCACTGTATAGATACACCT	1560
Q _y	1561	GCAAGGGGGCACAACCCACGTCGAGTTCGATGTTGTAAGTTCGTAAGAGTCAAA	1620
D _b	1561	GCAAGGGGGCACAACCCACGTCGAGTTCGATGTTGTAAGTTCGTAAGAGTCAAA	1620
Q _y	1621	TGGTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCAGAGGTACCCCATGT	1680
D _b	1621	TGGTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCAGAGGTACCCCATGT	1680
Q _y	1681	ATGGGATCTGATCTGGGCGCTCGGTGCATATGCTTTACATGTGTTAGTCGAGGTTAAA	1740
D _b	1681	ATGGGATCTGATCTGGGCGCTCGGTGCATATGCTTTACATGTGTTAGTCGAGGTTAAA	1740
Q _y	1741	AACGTCATAGGCCCGGACACGGGGACGTGTTTCTCTTTGAAAAACACCAATAATAC	1800
D _b	1741	AACGTCATAGGCCCGGACACGGGGACGTGTTTCTCTTTGAAAAACACCAATAATAC	1800
Q _y	1801	ATGGCGCCTATTACGGCCTACTCCCAACAGACGAGGCGCTACTTTGGCTGCATCATCT	1860
D _b	1801	ATGGCGCCTATTACGGCCTACTCCCAACAGACGAGGCGCTACTTTGGCTGCATCATCT	1860
Q _y	1861	AGCCTCACAGGCGGACAGGAACAGGTCTGAGGGGAGGTTCAGTGTCTCCACCGCA	1920
D _b	1861	AGCCTCACAGGCGGACAGGAACAGGTCTGAGGGGAGGTTCAGTGTCTCCACCGCA	1920
Q _y	1921	ACACATCTTTCTGGGACCTCGTCAATGGCGTGTGGTGTGTTGTTGTTGTTGTTGTTG	1980
D _b	1921	ACACATCTTTCTGGGACCTCGTCAATGGCGTGTGGTGTGTTGTTGTTGTTGTTGTTG	1980
Q _y	1981	GGCTCAAGACCTTTCGCGCCCAAGGGGCCCAATCACCCAAATGTACCAATGTGGAC	2040
D _b	1981	GGCTCAAGACCTTTCGCGCCCAAGGGGCCCAATCACCCAAATGTACCAATGTGGAC	2040
Q _y	2041	CAGGACCTCGTGGCTGGCAGCGCCCCCGGGCGGCTCTTGTGACACCATGCACCTGC	2100
D _b	2041	CAGGACCTCGTGGCTGGCAGCGCCCCCGGGCGGCTCTTGTGACACCATGCACCTGC	2100
Q _y	2101	GGCAGCTCGGACCTTTACTTGGTACAGGACATGCCGATGTCATTCGCTGCGCGCGG	2160

Db	2101	GGCAGCTCGGACCTTTACTTGGTCACGAGGCATGCCGATGTCATTCGGGTGCGCGCGG	2160
Qy	2161	GGCGACGACAGGGGAGCTACTCTCCCCAGGCCGCTCTCCTACTTGAAGGGCTCTTCG	2220
Db	2161	GGCGACGACAGGGGAGGCTACTCTCCCCAGGCCGCTCTCCTACTTGAAGGGCTCTTCG	2220
Qy	2221	GGCGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGTGC	2280
Db	2221	GGCGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGTGC	2280
Qy	2281	ACCCGAGGGTTCGGAAGCGGTGCACTTTGTACCCGTCGACTCTATGTAAGAACCACTATG	2340
Db	2281	ACCCGAGGGTTCGGAAGCGGTGCACTTTGTACCCGTCGACTCTATGTAAGAACCACTATG	2340
Qy	2341	CGGTCCCGGCTTTCACGGACAACCTGTCCTCCTCGGCCGTATCCGAGACATTCACAGGTG	2400
Db	2341	CGGTCCCGGCTTTCACGGACAACCTGTCCTCCTCGGCCGTATCCGAGACATTCACAGGTG	2400
Qy	2401	GCCATCTACACGCCCTTACTGTGTAGCGCAAGAGCACTAAGGTGCCGCTGGTATGCA	2460
Db	2401	GCCATCTACACGCCCTTACTGTGTAGCGCAAGAGCACTAAGGTGCCGCTGGTATGCA	2460
Qy	2461	GCCAAAGGTATAAGTGCTTCTGTAACCCGTGCTCGCCGCAACCTTAGTTCCTCGGG	2520
Db	2461	GCCAAAGGTATAAGTGCTTCTGTAACCCGTGCTCGCCGCAACCTTAGTTCCTCGGG	2520
Qy	2521	GCGTATGCTTAAGGCACATGCTATCGACCTTAACATCAGAAACCGGGTAAAGCAATC	2580
Db	2521	GCGTATGCTTAAGGCACATGCTATCGACCTTAACATCAGAAACCGGGTAAAGCAATC	2580
Qy	2581	ACCACGGTGCCGCCATCAGTACTCCACTATGGCAAGTTTCTTGCCGACGGTGTGTC	2640
Db	2581	ACCACGGTGCCGCCATCAGTACTCCACTATGGCAAGTTTCTTGCCGACGGTGTGTC	2640
Qy	2641	TCTGGGGCGCTATGACATCATATATGTGATGAGTGCCACTCAATGTACTCGACCACT	2700
Db	2641	TCTGGGGCGCTATGACATCATATATGTGATGAGTGCCACTCAATGTACTCGACCACT	2700
Qy	2701	ATCCTGGGCATCGGCACAGTCTCGACCAAGCGAGACGGCTGGAGCGCGACTCGTCGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGTCTCGACCAAGCGAGACGGCTGGAGCGCGACTCGTCGTG	2760
Qy	2761	CTCGCCACCGCTACGCCCTCGGGTACCGTGCCACATCCAAACATCGAGAGGTG	2820
Db	2761	CTCGCCACCGCTACGCCCTCGGGTACCGTGCCACATCCAAACATCGAGAGGTG	2820
Qy	2821	GCTGTGTCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATCGAGACCATC	2880
Db	2821	GCTGTGTCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGCACCTCATTTTCTGCCATTCCAAGAAAGATGTAGTCGCGCGG	2940
Db	2881	AAGGGGGGAGGCACCTCATTTTCTGCCATTCCAAGAAAGATGTAGTCGCGCGG	2940
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGCTTTGATCTCCGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGCTTTGATCTCCGTC	3000
Qy	3001	ATACCAATAGCGGAGACGTCATTTCTGCCATTCGAAGAAAGATGTAGTCGCGCTTACC	3060
Db	3001	ATACCAATAGCGGAGACGTCATTTCTGCCATTCGAAGAAAGATGTAGTCGCGCTTACC	3060
Qy	3061	GGCGATTTTCGACTGATCGACTGCAATATCATGTGTCAACAGACAGTCGACTTCAGC	3120
Db	3061	GGCGATTTTCGACTGATCGACTGCAATATCATGTGTCAACAGACAGTCGACTTCAGC	3120
Qy	3121	CTGGACCCGACCTTACCAATTTGAGACGACGACGCTGCCAAGACCGGCTGTCAACGCTCG	3180
Db	3121	CTGGACCCGACCTTACCAATTTGAGACGACGACGCTGCCAAGACCGGCTGTCAACGCTCG	3180
Qy	3181	CACGGGAGGACGAGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
Db	3181	CACGGGAGGACGAGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240

Db	5401	CTCATCGAGGCAACCTCTCTGTGGCGGAGAGATGGGCGGGAACATCACCCGCGTGAG	5460	
Qy	5461	TCAGAAATAGAGTAGTAATTTTGACATCTTCCGAGCCGCTCCAAAGCGAGAGAGATGAG	5520	
Db	5461		5520	
Qy	5521	AGGGAAGTATCCGTTCCGCGGAGATCTCTGGGAGGTCAGGAAATTCCTCTCGAGCGATG	5580	
Db	5521	AGGGAAGTATCCGTTCCGCGGAGATCTCTGGGAGGTCAGGAAATTCCTCTCGAGCGATG	5580	
Qy	5581	CCCATATGGGCGCGCCGAGTACAACTCTCACTGTTAGATCTCTGGGAAGGACCCGAGAC	5640	
Db	5581	CCCATATGGGCGCGCCGAGTACAACTCTCACTGTTAGATCTCTGGGAAGGACCCGAGAC	5640	
Qy	5641	TAGTCCCTCCAGTGTACACGGGTGTCCATTTGCCGCTGCCAAGGCCCTCCGATACCA	5700	
Db	5641	TAGTCCCTCCAGTGTACACGGGTGTCCATTTGCCGCTGCCAAGGCCCTCCGATACCA	5700	
Qy	5701	CTTCCACGGAGGAAGGAGCGGTTGCTGTGAGATCTACCGTGTCTTCTGCTTGGCG	5760	
Db	5701	CTTCCACGGAGGAAGGAGCGGTTGCTGTGAGATCTACCGTGTCTTCTGCTTGGCG	5760	
Qy	5761	GAGCTCGCACAAAGACCTTCGCGAGCTCCGAAATCGTGGCCCTCGACAGCGGCACGGCA	5820	
Db	5761	GAGCTCGCACAAAGACCTTCGCGAGCTCCGAAATCGTGGCCCTCGACAGCGGCACGGCA	5820	
Qy	5821	ACGCGCTCTCTGACACAGCCCTCCGACAGCGGAGACGCGGATCGGACGTTGAGTCGTAC	5880	
Db	5821	ACGCGCTCTCTGACACAGCCCTCCGACAGCGGAGACGCGGATCGGACGTTGAGTCGTAC	5880	
Qy	5881	TCCTTCCATGCCCCCTTTAGGGGAGCGCGGGGATCCGATCTCAGGACGGGTCTTGG	5940	
Db	5881	TCCTTCCATGCCCCCTTTAGGGGAGCGCGGGGATCCGATCTCAGGACGGGTCTTGG	5940	
Qy	5941	TCTACCGTAACGAGGAGGCTAGTCAGGACGCTGCTGCTGCTCGATGTCCTACACATGG	6000	
Db	5941	TCTACCGTAACGAGGAGGCTAGTCAGGACGCTGCTGCTGCTCGATGTCCTACACATGG	6000	
Qy	6001	ACAGGCGCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060	
Db	6001	ACAGGCGCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060	
Qy	6061	AGCAACTCTTGTCTCCGTACACAACTTTGTTATGCTACAACTCTCGAGCGCAAGC	6120	
Db	6061	AGCAACTCTTGTCTCCGTACACAACTTTGTTATGCTACAACTCTCGAGCGCAAGC	6120	
Qy	6121	CTGGGCGAGAAAGGTACCTTTGACAGCTGACAGTCTCGAGCGACCACTACCGGGAC	6180	
Db	6121	CTGGGCGAGAAAGGTACCTTTGACAGCTGACAGTCTCGAGCGACCACTACCGGGAC	6180	
Qy	6181	GTGCTCAAGGATGAAGCGGAGCGCTCCACAGTTAAGGCTAAACTTCTATCCGTTGGAG	6240	
Db	6181	GTGCTCAAGGATGAAGCGGAGCGCTCCACAGTTAAGGCTAAACTTCTATCCGTTGGAG	6240	
Qy	6241	GAGCTCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTTGTGGAGGACTTG	6300	
Db	6241	GAGCTCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTTGTGGAGGACTTG	6300	
Qy	6301	GAGCTCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTTGTGGAGGACTTG	6360	
Db	6301	GAGCTCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTTGTGGAGGACTTG	6360	
Qy	6361	CTGGAGACACTGAGACACCAATTTGACACCAATGAGGCTAAAGTGGGTTTCTGC	6420	
Db	6361	CTGGAGACACTGAGACACCAATTTGACACCAATGAGGCTAAAGTGGGTTTCTGC	6420	
Qy	6421	GTCCAAACAGAGAGGGGGCGGCAAGCGAGCTCGCTTATCGTATTTCCAGATTTGGGG	6480	
Db	6421	GTCCAAACAGAGAGGGGGCGGCAAGCGAGCTCGCTTATCGTATTTCCAGATTTGGGG	6480	
Qy	6481	GTTCGTGTGCGAGAAATGGCCCTTTAGGATGTGCTCTCCACCTCTCCCTCAGGCGGTG	6540	
Db	6481	GTTCGTGTGCGAGAAATGGCCCTTTAGGATGTGCTCTCCACCTCTCCCTCAGGCGGTG	6540	
Qy	6541	ATGGGCTCTTTCATACGGAATCCAAATATCTCTCTGAGACAGCGGTGCGAGTCTCTGTAAT	6600	
Db	6541	ATGGGCTCTTTCATACGGAATCCAAATATCTCTCTGAGACAGCGGTGCGAGTCTCTGTAAT	6600	
Qy	6601	GCTTGGAAAGCGAGAAATGCGCTATGCGCTTTCGCAATATGACACCGCTGTTTGTGACTCA	6660	
Db	6601	GCTTGGAAAGCGAGAAATGCGCTATGCGCTTTCGCAATATGACACCGCTGTTTGTGACTCA	6660	
Qy	6661	ACGGTCACTGAGATGACATCCGCTTTCGAGAGTCAATCTACCAATGTTGTGACTTGGCC	6720	
Db	6661	ACGGTCACTGAGATGACATCCGCTTTCGAGAGTCAATCTACCAATGTTGTGACTTGGCC	6720	
Qy	6721	CCCGAAGCGAGACAGCCCATTAAGCTCGCTTCACAGAGCGGCTTTACATCGGGGCCCCCTG	6780	
Db	6721	CCCGAAGCGAGACAGCCCATTAAGCTCGCTTCACAGAGCGGCTTTACATCGGGGCCCCCTG	6780	
Qy	6781	ACTAATTTCTAAAGGCGAGAACTCGGCTATCGCGGTGCGCGGAGCGGCTGTGTAAGC	6840	
Db	6781	ACTAATTTCTAAAGGCGAGAACTCGGCTATCGCGGTGCGCGGAGCGGCTGTGTAAGC	6840	
Qy	6841	ACCAGCTGCGGTAAATACCTCTCACATGTTTGAAGGCGCTCGGCTGTCTGAGCTGGC	6900	
Db	6841	ACCAGCTGCGGTAAATACCTCTCACATGTTTGAAGGCGCTCGGCTGTCTGAGCTGGC	6900	
Qy	6901	AACTCCAGACTGTCAGATGCTCGTATGCGGAGACGACCTTCTGTTATCTGTGAAGC	6960	
Db	6901	AACTCCAGACTGTCAGATGCTCGTATGCGGAGACGACCTTCTGTTATCTGTGAAGC	6960	
Qy	6961	GCGGGACCCACAGAGGACGAGCGGCTACGCGGCTTACGAGGCTATGATAGTATAC	7020	
Db	6961	GCGGGACCCACAGAGGACGAGCGGCTACGCGGCTTACGAGGCTATGATAGTATAC	7020	
Qy	7021	TCCTCCAAATGTGTCACTGCGGACGATGCTGCGGAGACGAGTGTGATGATGATGATG	7080	
Db	7021	TCCTCCAAATGTGTCACTGCGGACGATGCTGCGGAGACGAGTGTGATGATGATGATG	7080	
Qy	7081	TCCTCCAAATGTGTCACTGCGGACGATGCTGCGGAGACGAGTGTGATGATGATGATG	7140	
Db	7081	TCCTCCAAATGTGTCACTGCGGACGATGCTGCGGAGACGAGTGTGATGATGATGATG	7140	
Qy	7141	GACCCACCCACCCCTTGGCGGCGCTGCGGAGACGAGTGTGATGATGATGATGATG	7200	
Db	7141	GACCCACCCACCCCTTGGCGGCGCTGCGGAGACGAGTGTGATGATGATGATGATG	7200	
Qy	7201	TCCTGGCTAGGCAACATCATGATGATGATGATGATGATGATGATGATGATGATG	7260	
Db	7201	TCCTGGCTAGGCAACATCATGATGATGATGATGATGATGATGATGATGATGATG	7260	
Qy	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACCACTTGAAGGCTTGAATGATGATG	7320	
Db	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACCACTTGAAGGCTTGAATGATGATG	7320	
Qy	7321	ATCTAGGCGGCTGTACTTCCATTCAGGACCTTGAAGGCTTGAATGATGATGATGATG	7380	
Db	7321	ATCTAGGCGGCTGTACTTCCATTCAGGACCTTGAAGGCTTGAATGATGATGATGATG	7380	
Qy	7381	CATGGCTTGAAGGCTTCTTCTCCATGATGATGATGATGATGATGATGATGATGATG	7440	
Db	7381	CATGGCTTGAAGGCTTCTTCTCCATGATGATGATGATGATGATGATGATGATGATG	7440	
Qy	7441	TCATGCTCAGGAACTTGGGGTACCGGCTTTCGAGTCTGGAGATCGGGCCAGAAGT	7500	
Db	7441	TCATGCTCAGGAACTTGGGGTACCGGCTTTCGAGTCTGGAGATCGGGCCAGAAGT	7500	
Qy	7501	GTCCGCGCTAGGCTTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTTTC	7560	
Db	7501	GTCCGCGCTAGGCTTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTTTC	7560	
Qy	7561	AACTGGGCGAGTAAGGACCAAGCTCAACTCCTCAATCCCGCTGCTCCAGTTCGAT	7620	
Db	7561	AACTGGGCGAGTAAGGACCAAGCTCAACTCCTCAATCCCGCTGCTCCAGTTCGAT	7620	

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QY 7621 TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATATACAGCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATATACAGCCTGTCTCGT 7680
QY 7681 GCCGACCCCGCTGGTTCAATGCTGCTACTCTCTACTTCTCTAGGGTAGCATTCTAT 7740
Db 7681 GCCGACCCCGCTGGTTCAATGCTGCTACTCTCTACTTCTCTAGGGTAGCATTCTAT 7740
QY 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT 7800
Db 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT 7800
QY 7801 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
Db 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
QY 7921 TAGCTGTGAAGGTCGGTAGCGCGCTTGACTGCAGAGAGTGTGTAATCTGCTCTCTGC 7980
Db 7921 TAGCTGTGAAGGTCGGTAGCGCGCTTGACTGCAGAGAGTGTGTAATCTGCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 8
ID ABK91243 standard; DNA; 10690 BP.
XX AC ABK91243;
XX DT 15-NOV-2002 (first entry)
XX DE Hepatitis C virus vector construct pHCVNeo.17.m1.
KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX OS Hepatitis C virus.
XX OS Encephalomyocarditis virus.
XX OS Escherichia coli.
XX OS Enterobacteria phage T7.
XX OS Synthetic.

Key Location/Qualifiers
FH 5'UTR 1..341
FT /*tag= a
FT CDS 342..1181
FT /*tag= b
FT /product= "Core-neo fusion protein"
FT misc_signal 1190..1800
FT /*tag= c
FT /label= IRES
FT /note= "Internal ribosome entry site from BCMV"
FT CDS 1801..7758
FT /*tag= d
FT /product= "Polypotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
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FT /*tag= e
FT 3'UTR 7759..7991
FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /note= "Plasmid derived sequences"
XX PN W0200259321-A2.

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XX 01-AUG-2002.
PD
XX
XX 16-JAN-2002; 2002MO-EP000526.
PF
XX
XX 23-JAN-2001; 2001US-0263479P.
PR
XX
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
PA
XX
XX De Francesco R, Migliaccio G, Paonessa G;
PI MPI; 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
PT
XX
XX Example 1; Page; 69pp; English.
PS
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVNeo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in example 1
XX
SQ Sequence 10690 BP; 2333 A; 3046 C; 2908 G; 2403 T; 0 U; 0 Other;
Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAAGTACTG 60
Db 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAAGTACTG 60
QY 61 TCTTCAGCGAAGAGCGTCTAGCCATGGCGTTAGTAGTGTGTCGACGCTCCAGGAC 120
Db 61 TCTTCAGCGAAGAGCGTCTAGCCATGGCGTTAGTAGTGTGTCGACGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATTCGAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATTCGAG 180
QY 181 GAGCAGCGGGTCTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGGTGCCCC 240
Db 181 GAGCAGCGGGTCTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGGTGCCCC 240
QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTAGTCTGCTGATAG 300
Db 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTAGTCTGCTGATAG 300
QY 301 GTGCTTGGAGTGTGCCCCGGGAGGTCTCGTAGACCGGTGACACCATGACGAGATCTTAAC 360
Db 301 GTGCTTGGAGTGTGCCCCGGGAGGTCTCGTAGACCGGTGACACCATGACGAGATCTTAAC 360

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361 QY CTCAAGAAAAACCAAGGGCGCGCCATGATTGAACAGATGGATTGACGAGTTCTC 420
361 Db CTCAAGAAAAACCAAGGGCGCGCCATGATTGAACAGATGGATTGACGAGTTCTC 420
421 QY CGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATTCGGCTGCT 480
421 Db CGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATTCGGCTGCT 480
481 QY CTGATGCGCCCGTGTTCGGCTGTCAAGCAAGGGCGCCCGTTCCTTTTGTCAAGACCG 540
481 Db CTGATGCGCCCGTGTTCGGCTGTCAAGCAAGGGCGCCCGTTCCTTTTGTCAAGACCG 540
541 QY AACTGTCCGGTGCCCTGAAATGAATCTGACGACGAGGCGAGGCTATCGTGGCTGGCCA 600
541 Db AACTGTCCGGTGCCCTGAAATGAATCTGACGACGAGGCGAGGCTATCGTGGCTGGCCA 600
601 QY CGACGGGCGTTCCTTGGCGAGCTGTCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC 660
601 Db CGACGGGCGTTCCTTGGCGAGCTGTCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC 660
661 QY TGCTATTGGCGGAAGTGCCGGGCGAGGATCTCTGTCACTCACTTGTCTCTGCCGAGA 720
661 Db TGCTATTGGCGGAAGTGCCGGGCGAGGATCTCTGTCACTCACTTGTCTCTGCCGAGA 720
721 QY AAGTATCCATCATGGCTGATGCAATCGCGGCTGCACTACGCTTGATCCGGCTACCTGCC 780
721 Db AAGTATCCATCATGGCTGATGCAATCGCGGCTGCACTACGCTTGATCCGGCTACCTGCC 780
781 QY CATTTCGACCAACCAAGCAACATCGCATCGAGGAGCACGTACTTCGGATGGAAGCCGGTC 840
781 Db CATTTCGACCAACCAAGCAACATCGCATCGAGGAGCACGTACTTCGGATGGAAGCCGGTC 840
841 QY TTGTTCGATCAGGATGATCTGGAAGAGATCAGGGGCTCGCGCCAGCCGACGTTGCG 900
841 Db TTGTTCGATCAGGATGATCTGGAAGAGATCAGGGGCTCGCGCCAGCCGACGTTGCG 900
901 QY CCAGGCTCAAGCGCGCATGCGGAGGAGGATCTCGTGACACCATGGCGATGCT 960
901 Db CCAGGCTCAAGCGCGCATGCGGAGGAGGATCTCGTGACACCATGGCGATGCT 960
961 QY GCTTGGCGGAATCATGTGTGGAATGCGGCTTTCTGGAATCATGACCTGGCGCGGC 1020
961 Db GCTTGGCGGAATCATGTGTGGAATGCGGCTTTCTGGAATCATGACCTGGCGCGGC 1020
1021 QY TGGGTGTCGGACCGCTATCAGGACATAGCGTTGGCTACCGGATGATTTGCTGAAGAGC 1080
1021 Db TGGGTGTCGGACCGCTATCAGGACATAGCGTTGGCTACCGGATGATTTGCTGAAGAGC 1080
1081 QY TTGGGCGGATGGGCTGACCGCTTCCCTGCTGCTTTACGGTATCGCCGCTCCCGATTGCG 1140
1081 Db TTGGGCGGATGGGCTGACCGCTTCCCTGCTGCTTTACGGTATCGCCGCTCCCGATTGCG 1140
1141 QY AGCGCATCGCTTCTATCGCTTCTTGAAGGATCTTCTGAGTTTAAACAGACCAACG 1200
1141 Db AGCGCATCGCTTCTATCGCTTCTTGAAGGATCTTCTGAGTTTAAACAGACCAACG 1200
1201 QY GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGGC 1260
1201 Db GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGGC 1260
1261 QY CGAAGCGCTTGAATAAGGCGGTGTGCTATATGTTATTTTCCACCATATTG 1320
1261 Db CGAAGCGCTTGAATAAGGCGGTGTGCTATATGTTATTTTCCACCATATTG 1320
1321 QY CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGAAGGACTTCCT 1380
1321 Db CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGAAGGACTTCCT 1380
1381 QY AGGGGTCTTTCCTCTCGCCAAAGNATCGAAGGCTGTGTAATGTCTGTGAAGGAGCA 1440
1381 Db AGGGGTCTTTCCTCTCGCCAAAGNATCGAAGGCTGTGTAATGTCTGTGAAGGAGCA 1440
1441 QY GTTTCCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGTAGCGACCTTTTGCAGGACGG 1500

1441 QY GTTTCCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGTAGCGACCTTTTGCAGGACGG 1500
1501 QY AACCCCCCACCCTGGCGACAGGTGCTCTCGGCCAAAAAGCAGCGTGTATAGATACACT 1560
1501 Db AACCCCCCACCCTGGCGACAGGTGCTCTCGGCCAAAAAGCAGCGTGTATAGATACACT 1560
1561 QY GCAAAAGGGCGCAAAACCCAGTGCACGTTGTGAGTTCGATAGTGTGGAAGAGTCAAA 1620
1561 Db GCAAAAGGGCGCAAAACCCAGTGCACGTTGTGAGTTCGATAGTGTGGAAGAGTCAAA 1620
1621 QY TGGCTCTCTCAAGCGTATTCAACAAAGGGCTGGAAGGATGCCAGAGTACCCATTTGT 1680
1621 Db TGGCTCTCTCAAGCGTATTCAACAAAGGGCTGGAAGGATGCCAGAGTACCCATTTGT 1680
1681 QY ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGTTAAAA 1740
1681 Db ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGTTAAAA 1740
1741 QY AACGTCTAGGCCCCCGAAACCCAGGGACGTGGTTTTTCCCTTTGAAAAACACGATATACC 1800
1741 Db AACGTCTAGGCCCCCGAAACCCAGGGACGTGGTTTTTCCCTTTGAAAAACACGATATACC 1800
1801 QY ATGGCGCTATTACGGCTACTCCCAACAGACCGGAGGCTACTTTGGCTGCATCATCACT 1860
1801 Db ATGGCGCTATTACGGCTACTCCCAACAGACCGGAGGCTACTTTGGCTGCATCATCACT 1860
1861 QY AGCTCTCAGCGCGGACAGGAAACCCAGGTGCGAGGGGAGGTCCAAAGTGGTCTCCACGCA 1920
1861 Db AGCTCTCAGCGCGGACAGGAAACCCAGGTGCGAGGGGAGGTCCAAAGTGGTCTCCACGCA 1920
1921 QY ACACAATCTTCTTGGGACCTGCTCAATGGGCTGTGTTGGACTGTCTATCATGTGGCC 1980
1921 Db ACACAATCTTCTTGGGACCTGCTCAATGGGCTGTGTTGGACTGTCTATCATGTGGCC 1980
1981 QY GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
1981 Db GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
2041 QY CAGGACCTCTGCTGGCTGGCAAGCGCCCGCGGGCGGTCTTCTTGAACCAATGACCTTGC 2100
2041 Db CAGGACCTCTGCTGGCTGGCAAGCGCCCGCGGGCGGTCTTCTTGAACCAATGACCTTGC 2100
2101 QY GCGAGCTCGACCTTTTACTTGGTCAAGGCGATCGGATGCTATTCCGGTGGCGCGCGG 2160
2101 Db GCGAGCTCGACCTTTTACTTGGTCAAGGCGATCGGATGCTATTCCGGTGGCGCGCGG 2160
2161 QY GGCGACAGCAGGAGGAGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTTGC 2220
2161 Db GGCGACAGCAGGAGGAGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTTGC 2220
2221 QY GCGGCTCCACTGCTCTGCGCCCTCGGGGCAACGCTGTGGGCACTTTTCGGGCTGCGGTGC 2280
2221 Db GCGGCTCCACTGCTCTGCGCCCTCGGGGCAACGCTGTGGGCACTTTTCGGGCTGCGGTGC 2280
2281 QY ACCCAGAGGGTTCGAAAGCGGTGACCTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
2281 Db ACCCAGAGGGTTCGAAAGCGGTGACCTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
2341 QY CGGTCCCGGCTCTTCAAGGACAACTCGTCCCTCCGGCGGTACCGGAGCACTTCCAGGTG 2400
2341 Db CGGTCCCGGCTCTTCAAGGACAACTCGTCCCTCCGGCGGTACCGGAGCACTTCCAGGTG 2400
2401 QY GCGCATCTACACGCGCTCTGCTAGCGGCAAGGACCTAAGGTGCGGCTCGGTATGCA 2460
2401 Db GCGCATCTACACGCGCTCTGCTAGCGGCAAGGACCTAAGGTGCGGCTCGGTATGCA 2460
2461 QY GCGCAAGGATTAAGGTGCTTGTCTGAACCGCTCGGCGCCGACCCCTAGGTTTCGGG 2520
2461 Db GCGCAAGGATTAAGGTGCTTGTCTGAACCGCTCGGCGCCGACCCCTAGGTTTCGGG 2520
2521 QY GCGTATGCTTAAGGCAACATGGTATCGACCTTAACTCAAGACCGGGGTGAAGCAATC 2580

Db 2521 GCCTATATGCTAAGGCACATGGTATCGACCCCTAACATCGAAGCCCGGGTAAGSACCATC 2580
QY 2581 ACCACGGGTGCCCCCAATCAGTACTCACCTACTGCAAGTCTTCTGCGCAGCGTGGTTGC 2640
Db 2581 ACCACGGGTGCCCCCAATCAGTACTCACCTACTGCAAGTCTTCTGCGCAGCGTGGTTGC 2640
QY 2641 TCTGGGGGGCCCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGGGCCCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
QY 2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGACGCTGAGGCGGACTCGTGGT 2760
Db 2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGACGCTGAGGCGGACTCGTGGT 2760
QY 2761 CTGCGCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGTG 2820
Db 2761 CTGCGCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGTG 2820
QY 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC 2880
Db 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC 2880
QY 2881 AAGGGGGGAGSACCTCATTTCTTGCCATTCCAAAGAGAAATGTGATGAGTGCAGCTCGCGG 2940
Db 2881 AAGGGGGGAGSACCTCATTTCTTGCCATTCCAAAGAGAAATGTGATGAGTGCAGCTCGCGG 2940
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGATGATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGATGATCCGTC 3000
QY 3001 ATACCAACTAGCGGAGAGCTGATGCTGAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060
Db 3001 ATACCAACTAGCGGAGAGCTGATGCTGAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060
QY 3061 GGCATTTTCACTCAGTGATGACGCTCAATATGATGTCACCGAGAGTGCAGCTTACG 3120
Db 3061 GGCATTTTCACTCAGTGATGACGCTCAATATGATGTCACCGAGAGTGCAGCTTACG 3120
QY 3121 CTGGACCGGACTTACCATTTGAGACGACCGCTGCGCACAGCGCGGTGTACGCTCG 3180
Db 3121 CTGGACCGGACTTACCATTTGAGACGACCGCTGCGCACAGCGCGGTGTACGCTCG 3180
QY 3181 CAGCGGCGAGSAGGACTGGTGGGGGAGGATGGGCAATTAAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGCGAGSAGGACTGGTGGGGGAGGATGGGCAATTAAGGTTTGTGACTCCAGGA 3240
QY 3241 GAACGGCCCTCGGSCATGTTTGGATTCTCGGTTCTGTCAGAGTGTGAGCGGGCTGT 3300
Db 3241 GAACGGCCCTCGGSCATGTTTGGATTCTCGGTTCTGTCAGAGTGTGAGCGGGCTGT 3300
QY 3301 GCTTGTACGAGCTCAGCGCGCGGAGACTCTAGTTAGGTTGGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTACGAGCTCAGCGCGCGGAGACTCTAGTTAGGTTGGGGCTTACCTAAACACA 3360
QY 3361 CAGGGTTGCGGCTCTGCCAGGACCACTGGAGTCTGCGGAGAGCGTCTTTACAGGCTC 3420
Db 3361 CAGGGTTGCGGCTCTGCCAGGACCACTGGAGTCTGCGGAGAGCGTCTTTACAGGCTC 3420
QY 3421 ACCCATAGACGCCCATTTCTTGTCCAGACTAAGCAGSAGSAGACACTTCCCTTAC 3480
Db 3421 ACCCATAGACGCCCATTTCTTGTCCAGACTAAGCAGSAGSAGACACTTCCCTTAC 3480
QY 3481 CTGGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCAGCTCCATCGTGGGAC 3540
Db 3481 CTGGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCAGCTCCATCGTGGGAC 3540
QY 3541 CAAATGTGAAGTCTCTCATACGGCTAAAGGCTAACGCTGACGGGCCAACGCCCTGCTG 3600
Db 3541 CAAATGTGAAGTCTCTCATACGGCTAAAGGCTAACGCTGACGGGCCAACGCCCTGCTG 3600
QY 3601 TATAGSCTGGGAGCCGTTCAAACAGAGTTTACTACCACACACCCCATACCAAAATACATC 3660
Db 3601 TATAGSCTGGGAGCCGTTCAAACAGAGTTTACTACCACACACCCCATACCAAAATACATC 3660

QY 3661 ATGCGATGCAATGTCGCTGACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGA 3720
Db 3661 ATGCGATGCAATGTCGCTGACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGA 3720
QY 3721 GTCTTAGCAGCTCTGGCGCGGTATTGCTGCAACAGGAGCGTGTGTCATTGTGGGCGAG 3780
Db 3721 GTCTTAGCAGCTCTGGCGCGGTATTGCTGCAACAGGAGCGTGTGTCATTGTGGGCGAG 3780
QY 3781 ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGAGGAAGTCTTTACCGGGAGTTC 3840
Db 3781 ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGAGGAAGTCTTTACCGGGAGTTC 3840
QY 3841 GATGAGATGGAAGAGTGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAAGCTCGC 3900
Db 3841 GATGAGATGGAAGAGTGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAAGCTCGC 3900
QY 3901 GAACAATTCAAACAGAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCT 3960
Db 3901 GAACAATTCAAACAGAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCT 3960
QY 3961 GCTGCTCCGCTGGTGAATTCAGAGTGGGAGCCCTCGAAGCCTTCTGGCGGAAGCATATG 4020
Db 3961 GCTGCTCCGCTGGTGAATTCAGAGTGGGAGCCCTCGAAGCCTTCTGGCGGAAGCATATG 4020
QY 4021 TGGAAATTCATCAGCGGATACAATATTTAGCAGGCTTGTCCACTCTGCTCGCAACCCC 4080
Db 4021 TGGAAATTCATCAGCGGATACAATATTTAGCAGGCTTGTCCACTCTGCTGGCAACCCC 4080
QY 4081 CGCATAGCATCACTGATGGCAATTCAGGCTCTATCACAGCCGCTCACCAACCAAT 4140
Db 4081 CGCATAGCATCACTGATGGCAATTCAGGCTCTATCACAGCCGCTCACCAACCAAT 4140
QY 4141 ACCCTCTCTGTTTAAACATCTCGGGGAGTGGGTGGCGCCCACTTGTCTCCGAGCGCT 4200
Db 4141 ACCCTCTCTGTTTAAACATCTCGGGGAGTGGGTGGCGCCCACTTGTCTCCGAGCGCT 4200
QY 4201 GCTTCTGCTTTCGTTAGGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGGG 4260
Db 4201 GCTTCTGCTTTCGTTAGGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGTGCTCTGTGGATATTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGCC 4320
Db 4261 AAGTGCTCTGTGGATATTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGCC 4320
QY 4321 TTTAAGTCTATGAGCGCGGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT 4380
Db 4321 TTTAAGTCTATGAGCGCGGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT 4380
QY 4381 ATCTCTCCCTCGGCGCTTAGTCTGCGGGTCTGTTGCGCAGCGATCTGCGTCCGCGAC 4440
Db 4381 ATCTCTCCCTCGGCGCTTAGTCTGCGGGTCTGTTGCGCAGCGATCTGCGTCCGCGAC 4440
QY 4441 GTGGGCCAGGGGAGGGGCTGTCAGTGTGATGAACCGGCTGATAGGCTTCGTTCCGCG 4500
Db 4441 GTGGGCCAGGGGAGGGGCTGTCAGTGTGATGAACCGGCTGATAGGCTTCGTTCCGCG 4500
QY 4501 GSTTAAACAGCTCTCCCGCAGCGACTATGTGCTGAGAGCGAGCTGACGACGCTGCTACT 4560
Db 4501 GSTTAAACAGCTCTCCCGCAGCGACTATGTGCTGAGAGCGAGCTGACGACGCTGCTACT 4560
QY 4561 CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCCACAGTGGATCAAC 4620
Db 4561 CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCCACAGTGGATCAAC 4620
QY 4621 GAGGACTGCTCCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATGGATGCG 4680
Db 4621 GAGGACTGCTCCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATGGATGCG 4680
QY 4681 ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGGAGTTGCGGGA 4740
Db 4681 ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGGAGTTGCGGGA 4740

; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) HCV replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVneo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCGATGGGGCGACACCTCCACATAGATCACTCCCTGTGAGGAACACTG 60

DB 1 GCCAGCCCCGATGGGGCGACACCTCCACATAGATCACTCCCTGTGAGGAACACTG 60

QY 61 TCTTCACGCAAGAAGCGTGTAGCGGCTGTAGTATGATGATGCTGCTGAGCTCCAGGAC 120

DB 61 TCTTCACGCAAGAAGCGTGTAGCGGCTGTAGTATGATGATGCTGCTGAGCTCCAGGAC 120

QY 121 CCCCCCTCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATTGCCAG 180

DB 121 CCCCCCTCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATTGCCAG 180

QY 181 GACGACCGGTCTCTTCTTGATCAACCCGCTCAATCCCTGAGATTTGGCGTGGCCCC 240

DB 181 GACGACCGGTCTCTTCTTGATCAACCCGCTCAATCCCTGAGATTTGGCGTGGCCCC 240

QY 241 GCGAGATGTGTAGCGGAGTAGTGTGGTCCGGAAGCCCTGTGTACTCCCTGATAGG 300

DB 241 GCGAGATGTGTAGCGGAGTAGTGTGGTCCGGAAGCCCTGTGTACTCCCTGATAGG 300

QY 301 CTCAAGAAAAACCAAGGGCGCCATGATGTAACAAGATGGATTGCAACGATCTTAAC 360

DB 301 CTCAAGAAAAACCAAGGGCGCCATGATGTAACAAGATGGATTGCAACGATCTTAAC 360

QY 361 CTCAAGAAAAACCAAGGGCGCCATGATGTAACAAGATGGATTGCAACGATCTTAAC 420

DB 361 CTCAAGAAAAACCAAGGGCGCCATGATGTAACAAGATGGATTGCAACGATCTTAAC 420

QY 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGATGAGGCAACAGACATTCGGCTGCT 480

DB 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGATGAGGCAACAGACATTCGGCTGCT 480

QY 481 CTGATGCGCGCTGTTCGGCTGTCTAGCGGCGGCGCGGCTCTTTTGTCAAGACCG 540

DB 481 CTGATGCGCGCTGTTCGGCTGTCTAGCGGCGGCGCGGCTCTTTTGTCAAGACCG 540

QY 541 ACCTGTCCGGTCCCTGTAATGAATCTGAGGAAGAGCGCGGCTATCGTGGCTGGCCA 600

DB 541 ACCTGTCCGGTCCCTGTAATGAATCTGAGGAAGAGCGCGGCTATCGTGGCTGGCCA 600

QY 601 CGACGGGCTTCTTTCGGCAGCTGTCTGAGGCTGTGCTGAGGCTGAGGCTGAGGCTGGC 660

DB 601 CGACGGGCTTCTTTCGGCAGCTGTCTGAGGCTGTGCTGAGGCTGAGGCTGAGGCTGGC 660

QY 661 TGTCTATGGCGAAGTGGCGGCGAGGATCTCTGTCTATCTCACTTGTCTCTGCGCGAGA 720

DB 661 TGTCTATGGCGAAGTGGCGGCGAGGATCTCTGTCTATCTCACTTGTCTCTGCGCGAGA 720

QY 721 AAGTATCCATCATGGCTGATGATGGCGGCTGATAGCTGATAGCTGATAGCTGATAGCTGCC 780

DB 721 AAGTATCCATCATGGCTGATGATGGCGGCTGATAGCTGATAGCTGATAGCTGATAGCTGCC 780

781 CATTGACCAACAAGCGAAACATCGCATCGAGCGACAGTCTCGGATGGAAGCGGTC 840

781 CATTGACCAACAAGCGAAACATCGCATCGAGCGACAGTCTCGGATGGAAGCGGTC 840

841 TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG 900

841 TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG 900

901 CCAGGCTCAAGCGCGCATGCCCGGCGAGGATCTCGTGTGACCCATGCGGATGCT 960

901 CCAGGCTCAAGCGCGCATGCCCGGCGAGGATCTCGTGTGACCCATGCGGATGCT 960

961 GTTGGCGAATATCATGTTGGAATGCGGCTTTTCTGATTCATCGACTGTGGCGGC 1020

961 GTTGGCGAATATCATGTTGGAATGCGGCTTTTCTGATTCATCGACTGTGGCGGC 1020

1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTGTGGTACCCGCTGATATTGCTGAAGAGC 1080

1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCTGTGGTACCCGCTGATATTGCTGAAGAGC 1080

1081 TTGGCGCGAATGGGCTGACCGCTTCTGAGGATTTCTTGAAGTTTAAACAGACCAACAG 1140

1081 TTGGCGCGAATGGGCTGACCGCTTCTGAGGATTTCTTGAAGTTTAAACAGACCAACAG 1140

1141 AGCGCATCGCTTCTATCGGCTTCTTGAAGGATTTCTTGAAGTTTAAACAGACCAACAG 1200

1141 AGCGCATCGCTTCTATCGGCTTCTTGAAGGATTTCTTGAAGTTTAAACAGACCAACAG 1200

1201 GTTTCCTCTGAGCGGATCAATTCGCGCTTCTCCCTCCCGCTCCCGCTCCCGCTCCCGCT 1260

1201 GTTTCCTCTGAGCGGATCAATTCGCGCTTCTCCCTCCCGCTCCCGCTCCCGCTCCCGCT 1260

1261 CGAAGCGCTTGAAGTAAAGCGGCTGTGCTTGTCTATGATTTTCCACCATATG 1320

1261 CGAAGCGCTTGAAGTAAAGCGGCTGTGCTTGTCTATGATTTTCCACCATATG 1320

1321 CCGTCTTTGGCAATGTGAGGCGCGGAACTCGGCTTCTTCTGACGAGCATTCCT 1380

1321 CCGTCTTTGGCAATGTGAGGCGCGGAACTCGGCTTCTTCTGACGAGCATTCCT 1380

1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGCTCTGTAATGCTGTAAGGAAGCA 1440

1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGCTCTGTAATGCTGTAAGGAAGCA 1440

1441 GTTCTCTGGAAGCTTCTGGAAGCAAAACAGCTCTGTAGGACCCCTTTGAGGAGCGG 1500

1441 GTTCTCTGGAAGCTTCTGGAAGCAAAACAGCTCTGTAGGACCCCTTTGAGGAGCGG 1500

1501 AACCCCCCCTGCGGACAGGTCCTCGCGCCAAAGCAACGTCGTATATAAGATACCT 1560

1501 AACCCCCCCTGCGGACAGGTCCTCGCGCCAAAGCAACGTCGTATATAAGATACCT 1560

1561 GCMAAGGCGGCAACACCCAGTGCCTCGCGCCAAAGCAACGTCGTATATAAGATACCT 1620

1561 GCMAAGGCGGCAACACCCAGTGCCTCGCGCCAAAGCAACGTCGTATATAAGATACCT 1620

1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGMAAGGATGCGGAGAGTACCCATTGT 1680

1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGMAAGGATGCGGAGAGTACCCATTGT 1680

1681 ATGGGATCTGATCTGGGCTCGGTGCACTGTTTACATGTTTGTAGTTCGAGGTTTAAA 1740

1681 ATGGGATCTGATCTGGGCTCGGTGCACTGTTTACATGTTTGTAGTTCGAGGTTTAAA 1740

1741 AACGCTTAGGCGGCGGAAACACCGGGGAGCTGGTTCCTTTGAAAAACAGCATATACC 1800

1741 AACGCTTAGGCGGCGGAAACACCGGGGAGCTGGTTCCTTTGAAAAACAGCATATACC 1800

1801 ATGGGCGCTATTACGCGCTTCTCCCAACAGAGCGGAGGCTTCTTGGCTGCATCATCACT 1860

1801 ATGGGCGCTATTACGCGCTTCTCCCAACAGAGCGGAGGCTTCTTGGCTGCATCATCACT 1860

1861 AGGCTCACAGCGCGGAGCAAGAACAGGTCGAGGGGGAGGTCCTCAAGTGTCTCCACGCA 1920

Db 1861 AGCTTACAGCGCGGACAGAAACAGTGCAGGGGGAGTCCAAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAATCTTCTGGCGACCTCGGTCAATGGCGGTGTGTGGACTGTCTATCATGTGGCC 1980
Db 1921 ACACAATCTTCTGGCGACCTCGGTCAATGGCGGTGTGTGGACTGTCTATCATGTGGCC 1980
QY 1981 GCGTCAAGACCCCTTGGCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
Db 1981 GCGTCAAGACCCCTTGGCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
QY 2041 CAGGACTCGTGGCTGGCAAGCGCCCGGGGGCGGTCTTGTACACCATGTGCACCTGC 2100
Db 2041 CAGGACTCGTGGCTGGCAAGCGCCCGGGGGCGGTCTTGTACACCATGTGCACCTGC 2100
QY 2101 GGCAGCTCGGACTTACTTGTGTACAGAGGCATGCCGATGTCAATCCGGTGGCGGGCGG 2160
Db 2101 GGCAGCTCGGACTTACTTGTGTACAGAGGCATGCCGATGTCAATCCGGTGGCGGGCGG 2160
QY 2161 GCGGACAGCAGGGGAGCTACTCTCCCGACGGCCGCTCTCCTACTTGAAGGCTCTTCG 2220
Db 2161 GCGGACAGCAGGGGAGCTACTCTCCCGACGGCCGCTCTCCTACTTGAAGGCTCTTCG 2220
QY 2221 GCGGTGCCACTGCTCTGCCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTC 2280
Db 2221 GCGGTGCCACTGCTCTGCCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTC 2280
QY 2281 ACCGAGGGGTTCGAAAGCGGTGGACTTGTACCCGCTCGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGGTTCGAAAGCGGTGGACTTGTACCCGCTCGAGTCTATGGAACCACTATG 2340
QY 2341 CGGTCCCCTGCTTTCACGGCAAACTCGCTCCGCGCGTACCGACACATTCACGGTG 2400
Db 2341 CGGTCCCCTGCTTTCACGGCAAACTCGCTCCGCGCGTACCGACACATTCACGGTG 2400
QY 2401 GCCCATCTACACGCCCTACTGTGTAGCGGACAGACATAAGTGCAGGTGCCGTGCGTATGCA 2460
Db 2401 GCCCATCTACACGCCCTACTGTGTAGCGGACAGACATAAGTGCAGGTGCCGTGCGTATGCA 2460
QY 2461 GCCAAGGGTATAAGGTGCTTGTCTGAAACCGCTCCGTCGCGCCACCCCTAGGTTTCGGG 2520
Db 2461 GCCAAGGGTATAAGGTGCTTGTCTGAAACCGCTCCGTCGCGCCACCCCTAGGTTTCGGG 2520
QY 2521 GCGTATATGTCTAAGGCACATGTGTATGACCCCTAACATCAGAACCGGGTAAAGACCATC 2580
Db 2521 GCGTATATGTCTAAGGCACATGTGTATGACCCCTAACATCAGAACCGGGTAAAGACCATC 2580
QY 2581 ACCACGGGTGCCCCATCAGTACTCCACCTATGGCAAGTTCTTGGCGAGGTGGTTC 2640
Db 2581 ACCACGGGTGCCCCATCAGTACTCCACCTATGGCAAGTTCTTGGCGAGGTGGTTC 2640
QY 2641 TCTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
QY 2701 ATCTGGGATCGGCACAGTCTCTGGAACAAGCGGAGACGCTGGAGCGCACTCGTCTG 2760
Db 2701 ATCTGGGATCGGCACAGTCTCTGGAACAAGCGGAGACGCTGGAGCGCACTCGTCTG 2760
QY 2761 CTGCGCACCGCTACGCTCTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG 2820
Db 2761 CTGCGCACCGCTACGCTCTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG 2820
QY 2821 GCTGTGTACGACTGAGAAATCCCTTTTATGGCAAGGCCATCCCCATCGAGACCATC 2880
Db 2821 GCTGTGTACGACTGAGAAATCCCTTTTATGGCAAGGCCATCCCCATCGAGACCATC 2880
QY 2881 AAGGGGGGAGGACCTCATTTTCTGCGCATTCAGAAGAAATGTGATGAGTCTGCCGCG 2940
Db 2881 AAGGGGGGAGGACCTCATTTTCTGCGCATTCAGAAGAAATGTGATGAGTCTGCCGCG 2940
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000

Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000
QY 3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGGAACGCTCTAATGACGGGCTTTACC 3060
Db 3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGGAACGCTCTAATGACGGGCTTTACC 3060
QY 3061 GCGGATTTTCGACTCAGTGTATCGACTCAATATCATGTGTCAACGAGACAGTCGACTTCAG 3120
Db 3061 GCGGATTTTCGACTCAGTGTATCGACTCAATATCATGTGTCAACGAGACAGTCGACTTCAG 3120
QY 3121 CTGGACCCGACCTTACCATTTGAGAGACGACGCTGCCACAGACGGGTGTACGCTCG 3180
Db 3121 CTGGACCCGACCTTACCATTTGAGAGACGACGCTGCCACAGACGGGTGTACGCTCG 3180
QY 3181 CAGCGCGAGGACGAGTGTAGGGGACGATGGGCATTTACAGGTTTGTGATCTCCAGGA 3240
Db 3181 CAGCGCGAGGACGAGTGTAGGGGACGATGGGCATTTACAGGTTTGTGATCTCCAGGA 3240
QY 3241 GAACGGCCCTCGGGCATGTTCCATTTCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
Db 3241 GAACGGCCCTCGGGCATGTTCCATTTCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
QY 3301 GCTTGTGTACGAGCTCAGCGCCCGCGAGACCTCTGGAGAGGCTCTTGTACAGGCTTC 3360
Db 3301 GCTTGTGTACGAGCTCAGCGCCCGCGAGACCTCTGGAGAGGCTCTTGTACAGGCTTC 3360
QY 3361 CAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTCTCTGGAGAGGCTCTTGTACAGGCTTC 3420
Db 3361 CAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTCTCTGGAGAGGCTCTTGTACAGGCTTC 3420
QY 3421 ACCCACATAGAGGCCCATTTCTTGTCCAGACTAAGAGGAGGAGAGCAACTTCCCTTAC 3480
Db 3421 ACCCACATAGAGGCCCATTTCTTGTCCAGACTAAGAGGAGGAGAGCAACTTCCCTTAC 3480
QY 3481 CTGTGTAGCATACAGGCTACCGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
Db 3481 CTGTGTAGCATACAGGCTACCGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
QY 3541 CAAATGTGGAAAGTGTCTCATACGCTAAAGCTTACGCTGACAGGCGCCAAACGCCCTGCTG 3600
Db 3541 CAAATGTGGAAAGTGTCTCATACGCTAAAGCTTACGCTGACAGGCGCCAAACGCCCTGCTG 3600
QY 3601 TATAGGCTGGAGCGGCTTCAAAACAGGTTTACTACGACACACCCCAATAACAAATACATC 3660
Db 3601 TATAGGCTGGAGCGGCTTCAAAACAGGTTTACTACGACACACCCCAATAACAAATACATC 3660
QY 3661 ATGCGATGCAATGTCGGCTGACCTGAGGTGTGCGCAGGACCTGGGTCTGTGGTAGGGGA 3720
Db 3661 ATGCGATGCAATGTCGGCTGACCTGAGGTGTGCGCAGGACCTGGGTCTGTGGTAGGGGA 3720
QY 3721 GTCTTAGCAGCTCTGGCGCGGTATTTGCTGACAAACAGGCGGTGTCTTGTGGGCGAGG 3780
Db 3721 GTCTTAGCAGCTCTGGCGCGGTATTTGCTGACAAACAGGCGGTGTCTTGTGGGCGAGG 3780
QY 3781 ATCATCTGTCCGAAAGCGGCGCATATTTCCGACAGGGAAGTCTTTTACCAGGAGTTC 3840
Db 3781 ATCATCTGTCCGAAAGCGGCGCATATTTCCGACAGGGAAGTCTTTTACCAGGAGTTC 3840
QY 3841 GATGAGATGGAAGAGTGGCGCTCAGACCTCCCTTACATGCAACAGGGAATTCGACTCGCC 3900
Db 3841 GATGAGATGGAAGAGTGGCGCTCAGACCTCCCTTACATGCAACAGGGAATTCGACTCGCC 3900
QY 3901 GAACAATTCAAACAGAGGCAATTCGGGTGTCTGCAAAACAGCCACCAAGCAAGCGGAGCT 3960
Db 3901 GAACAATTCAAACAGAGGCAATTCGGGTGTCTGCAAAACAGCCACCAAGCAAGCGGAGCT 3960
QY 3961 GCTGTCTCCGTTGGTGAATCCAAAGTGGCGGACCCCTCGAAGCTTCTGTGGCGAAGCATATG 4020
Db 3961 GCTGTCTCCGTTGGTGAATCCAAAGTGGCGGACCCCTCGAAGCTTCTGTGGCGAAGCATATG 4020
QY 4021 TGGAAATTTTCATCAGCGGGATACAAATTTTAGCAGGCTTGTCCACTCTGCTGGCAACCCC 4080
Db 4021 TGGAAATTTTCATCAGCGGGATACAAATTTTAGCAGGCTTGTCCACTCTGCTGGCAACCCC 4080

Qy	4081	GC	GT	AG	CA	TCA	CTG	AT	TCA	AG	CC	TCT	TAT	C	A	C	A	G	C	C	C	G	T	C	A	C	C	C	A	A	C	A	T	4140				
Db	4081	GC	GA	T	GA	T	CA	T	CA	AG	CC	T	T	A	T	C	A	C	A	G	C	C	G	T	C	A	C	C	C	A	A	C	A	T	4140			
Qy	4141	ACC	CT	CT	CT	T	T	A	A	C	A	T	C	T	T	G	G	G	G	A	T	G	G	T	G	G	C	C	C	C	C	C	A	T	4200			
Db	4141	ACC	CT	CT	CT	T	T	A	A	C	A	T	C	T	T	G	G	G	G	A	T	G	G	T	G	G	C	C	C	C	C	C	A	T	4200			
Qy	4201	G	C	T	T	G	T	T	G	T	A	G	C	C	T	G	T	A	G	C	C	T	G	T	A	G	C	C	T	G	T	A	G	C	T	4260		
Db	4201	G	C	T	T	G	T	T	G	T	A	G	C	C	T	G	T	A	G	C	C	T	G	T	A	G	C	C	T	G	T	A	G	C	T	4260		
Qy	4261	A	A	G	T	G	C	T	T	G	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	4320			
Db	4261	A	A	G	T	G	C	T	T	G	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	4320			
Qy	4321	T	T	T	A	A	G	T	C	A	T	A	G	C	C	T	T	C	C	A	C	C	G	A	G	A	C	C	T	T	A	C	T	A	C	T	4380	
Db	4321	T	T	T	A	A	G	T	C	A	T	A	G	C	C	T	T	C	C	A	C	C	G	A	G	A	C	C	T	T	A	C	T	A	C	T	4380	
Qy	4381	A	T	C	T	T	C	C	T	T	G	C	C	T	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	4440		
Db	4381	A	T	C	T	T	C	C	T	T	G	C	C	T	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	4440		
Qy	4441	G	T	G	G	C	C	A	G	G	G	G	G	T	G	T	G	C	A	T	G	A	T	G	A	T	G	A	T	G	C	T	T	T	T	T	4500	
Db	4441	G	T	G	G	C	C	A	G	G	G	G	G	T	G	T	G	C	A	T	G	A	T	G	A	T	G	A	T	G	C	T	T	T	T	T	4500	
Qy	4501	G	G	T	A	A	C	C	A	C	G	T	C	T	C	C	C	C	C	A	C	C	T	A	T	G	T	G	C	T	A	G	A	G	C	T	4560	
Db	4501	G	G	T	A	A	C	C	A	C	G	T	C	T	C	C	C	C	C	A	C	C	T	A	T	G	T	G	C	T	A	G	A	G	C	T	4560	
Qy	4561	C	A	G	A	T	C	T	C	T	A	G	T	T	A	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	4620	
Db	4561	C	A	G	A	T	C	T	C	T	A	G	T	T	A	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	4620	
Qy	4621	G	A	G	A	C	T	G	T	C	C	A	G	C	A	T	G	T	C	C	A	G	C	A	T	G	T	C	C	A	G	C	A	T	G	A	T	4680
Db	4621	G	A	G	A	C	T	G	T	C	C	A	G	C	A	T	G	T	C	C	A	G	C	A	T	G	T	C	C	A	G	C	A	T	G	A	T	4680
Qy	4681	A	C	G	T	T	G	A	C	T	T	A</																										

Db 6241 GAAGCCTGTAAAGCTGACGCCCCACATCTTCGGCAGATCTAAATTTGGCTATATGGGCAAAAG 6300
QY 6301 GAGCTCGGAACCTATTCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTGGAAGGACTTG 6360
Db 6301 GAGCTCGGAACCTATTCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTGGAAGGACTTG 6360
QY 6361 CTGGAGAGACTGAGACACCAATTTGACACCAATCATGGCAAAAATAGAGTTTTCTGC 6420
Db 6361 CTGGAGAGACTGAGACACCAATTTGACACCAATCATGGCAAAAATAGAGTTTTCTGC 6420
QY 6421 GTCCAAACAGAGAAAGGGGCGCCAGAGCCAGCTCGCTTATCGTATTCAGATTTGGGG 6480
Db 6421 GTCCAAACAGAGAAAGGGGCGCCAGAGCCAGCTCGCTTATCGTATTCAGATTTGGGG 6480
QY 6481 GTTCGTGTGTGGAGAAAATGGCCCTTTTACGATGTGGTCTCCACCTCTCCCTCAGGCCGTG 6540
Db 6481 GTTCGTGTGTGGAGAAAATGGCCCTTTTACGATGTGGTCTCCACCTCTCCCTCAGGCCGTG 6540
QY 6541 ATGGGCTCTTCATACGGATTCGAATCTCTCTGGACAGCGGTGAGTTCTGTGTGAAT 6600
Db 6541 ATGGGCTCTTCATACGGATTCGAATCTCTCTGGACAGCGGTGAGTTCTGTGTGAAT 6600
QY 6601 GCCTGGAAGCGAGAAATGCGCTATGGGCTTCGCATATGACACCGCTGTTTGACTCA 6660
Db 6601 GCCTGGAAGCGAGAAATGCGCTATGGGCTTCGCATATGACACCGCTGTTTGACTCA 6660
QY 6661 ACGGTCACTGAGAATGACATCCGTGTGTAGGAGTCAATCTACCAATGTTGACCTGGCC 6720
Db 6661 ACGGTCACTGAGAATGACATCCGTGTGTAGGAGTCAATCTACCAATGTTGACCTGGCC 6720
QY 6721 CCCGAAGCCAGACAGCCATAGGTGCTGTCAGAGCGGCTTTACATCGGGGCCCCCTG 6780
Db 6721 CCCGAAGCCAGACAGCCATAGGTGCTGTCAGAGCGGCTTTACATCGGGGCCCCCTG 6780
QY 6781 ACTAATTTCTAAAGGCGAGAACTGCGCTATCGCGGTGCGCGGCTGCGGCTGCGAGCTGCG 6840
Db 6781 ACTAATTTCTAAAGGCGAGAACTGCGCTATCGCGGTGCGCGGCTGCGGCTGCGAGCTGCG 6840
QY 6841 ACCAGTCCGGTAAACCTCACATGTTACTTGAAGGCGGCTGCGGCTGCGAGCTGCG 6900
Db 6841 ACCAGTCCGGTAAACCTCACATGTTACTTGAAGGCGGCTGCGGCTGCGAGCTGCG 6900
QY 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGACCTTGTGTTATCTGTGAAAGC 6960
Db 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGACCTTGTGTTATCTGTGAAAGC 6960
QY 6961 GCGGGACCCAAAGAGGAGCGAGCGCTACCGGCTTACGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCAAAGAGGAGCGAGCGCTACCGGCTTACGAGGCTATGACTAGATAC 7020
QY 7021 TCTGCCCCCTTGGGACCCGCCCCAAACCAATACGACTTGGAGTTGATAAATCATGC 7080
Db 7021 TCTGCCCCCTTGGGACCCGCCCCAAACCAATACGACTTGGAGTTGATAAATCATGC 7080
QY 7081 TCTCCATGTTGTCAGTTCGCGCAGATGCTATGCGGAGACGACCTTGTGTTATCTCACCCGT 7140
Db 7081 TCTCCATGTTGTCAGTTCGCGCAGATGCTATGCGGAGACGACCTTGTGTTATCTCACCCGT 7140
QY 7141 GACCCACCAACCCCTTGGCGGCGCTGCGGAGACAGTACACACTCCAGTCAAT 7200
Db 7141 GACCCACCAACCCCTTGGCGGCGCTGCGGAGACAGTACACACTCCAGTCAAT 7200
QY 7201 TCTGGCTAGGCAACATCATGATGCGGCCACCTTGTGGCAAGGATGATCCTGATG 7260
Db 7201 TCTGGCTAGGCAACATCATGATGCGGCCACCTTGTGGCAAGGATGATCCTGATG 7260
QY 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAAACACTTGAAGGAGCCCTAGATTTGTCAG 7320
Db 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAAACACTTGAAGGAGCCCTAGATTTGTCAG 7320
QY 7321 ATCTACGGGCGCTGTACTCCATGAGCCACTTGACCTACTCAGATCATTTCAACGACTC 7380

Db 7321 ATCTACGGGCGCTGTACTCCATTTAGGACCACTTGACCTACTCAGATCATTTCAACGACTC 7380
QY 7381 CATGGCCTTAGCGCATTTTTCATCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Db 7381 CATGGCCTTAGCGCATTTTTCATCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
QY 7441 TCATGCTCAGGAAACTTGGGTACCGCTTGGAGTCTGGAGATCTGGGCGAGAAGT 7500
Db 7441 TCATGCTCAGGAAACTTGGGTACCGCTTGGAGTCTGGAGATCTGGGCGAGAAGT 7500
QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGCGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCCGCGCTAGGCTACTGTCCAGGGGCGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
QY 7561 AACTGGGCAATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAGTTGGAT 7620
Db 7561 AACTGGGCAATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAGTTGGAT 7620
QY 7621 TTATCCAGCTGTTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTGT 7680
Db 7621 TTATCCAGCTGTTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTGT 7680
QY 7681 GCCGACCCCGCTGTTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTGT 7740
Db 7681 GCCGACCCCGCTGTTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTGT 7740
QY 7741 CTACTCCCAACCGATGAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
Db 7741 CTACTCCCAACCGATGAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TAGCTGTAAAGGTCCTGAGCGCTTGTGACTGCGAGAGTCTGATCTGGCTCTCTGCG 7980
Db 7921 TAGCTGTAAAGGTCCTGAGCGCTTGTGACTGCGAGAGTCTGATCTGGCTCTCTGCG 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 10
ADP86264
ID ADP86264 standard; DNA; 11313 BP.
XX AC ADP86264;
XX DT 23-SEP-2004 (first entry)
XX DE Hepatitis C virus Con-1 replicon I377/NS3-3' plasmid DNA.
XX KW Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;
XX OS ds.
XX OS Hepatitis C virus.
XX PN WO200405216-A2.
XX PD 01-JUL-2004.
XX PF 12-DEC-2003; 2003WO-US039722.
XX PR 13-DEC-2002; 2002US-0433303P.
XX PA (FOXC-) FOX CHASE CANCER CENT.
XX PI Zhu Q, Guo J, Seeger C;

XX	WPI; 2004-488079/46.
DR	GENBANK; AJ242652.
XX	
PT	New cell-line that replicates hepatitis C virus (HCV), where the cell
PT	line is selected from a non-human cell line and a human non-hepatic cell
PT	line, useful for identifying anti-HCV agents for treating HCV infections.
XX	
XX	Example III; SEQ ID NO 1; 130pp; English.
PS	
XX	
CC	The present invention provides hepatitis C virus (HCV) replication cells
CC	and cell lines derived from human non-hepatic cells or non-human cells
CC	The invention is useful for identifying anti-HCV agents for treating HCV
CC	infections. The present sequence is hepatitis C virus Con-1 replicon
CC	C 1377/NS3-3' plasmid DNA.
XX	
XX	Sequence 11313 BP; 2347 A; 3334 C; 3152 G; 2480 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 7990.4; DB 12; Length 11313;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 7991; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 GCCAGCCCCGANTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACACTG 60
Db	1 GCCAGCCCCGANTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACACTG 60
Qy	61 TCCTCAGCGAAGACGCTCTAGCCATGCGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
Db	61 TCCTCAGCGAAGACGCTCTAGCCATGCGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
Qy	121 CCCCCCTCCGGGAGAGCATAGTGGTCTCGGGAACCGGTGAGTACACCGGAATTGCCAG 180
Db	121 CCCCCCTCCGGGAGAGCATAGTGGTCTCGGGAACCGGTGAGTACACCGGAATTGCCAG 180
Qy	181 GACGACCGGGTCCTTTCTTGATCAACCCGCTCAATGCTCGAGATTGGCGCTGCCCCC 240
Db	181 GACGACCGGGTCCTTTCTTGATCAACCCGCTCAATGCTCGAGATTGGCGCTGCCCCC 240
Qy	241 GCGAGACTGCTAGCGGAGTAGTGTGGTTCGGAAAGCCCTTGTGCTACTGCCCTGATAGG 300
Db	241 GCGAGACTGCTAGCGGAGTAGTGTGGTTCGGAAAGCCCTTGTGCTACTGCCCTGATAGG 300
Qy	301 GTGCTTGGAGTGCCTCCGGGAGTCTCGTAGACCTGCACCATGAGCACGAATCCTAAAC 360
Db	301 GTGCTTGGAGTGCCTCCGGGAGTCTCGTAGACCTGCACCATGAGCACGAATCCTAAAC 360
Qy	361 CTCAAAGAAAAACCAAAGGCGCGCCATGATTGAACAAAGATGAGTGCACGAGTCTTC 420
Db	361 CTCAAAGAAAAACCAAAGGCGCGCCATGATTGAACAAAGATGAGTGCACGAGTCTTC 420
Qy	421 CGCGCGTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGACAATTCGCTGCT 480
Db	421 CGCGCGTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGACAATTCGCTGCT 480
Qy	481 CTGATGCCCGCTGTTCCGCTGTGAGCGAGGCGCCCGTCTTTTGTTCAGACCG 540
Db	481 CTGATGCCCGCTGTTCCGCTGTGAGCGAGGCGCCCGTCTTTTGTTCAGACCG 540
Qy	541 ACCTGTCCGGTCCCTGAATGAATGACGAGACGAGGCGGCTATCGTGGCTGGCCA 600
Db	541 ACCTGTCCGGTCCCTGAATGAATGACGAGACGAGGCGGCTATCGTGGCTGGCCA 600
Qy	601 CGACGGCGCTTCTTCGCGAGCTGTCTCGACCTTGTCACTGAAGCGGAAAGGACTGCG 660
Db	601 CGACGGCGCTTCTTCGCGAGCTGTCTCGACCTTGTCACTGAAGCGGAAAGGACTGCG 660
Qy	661 TGCTATTGGCGAAGTCCCGGGGACGAGATCTCTGTCACTACCTTGTCTCTCCGCGA 720
Db	661 TGCTATTGGCGAAGTCCCGGGGACGAGATCTCTGTCACTACCTTGTCTCTCCGCGA 720
Qy	721 AAGTATCCATGAGTGTGATGATCGGCGGTGATACGCTTGTATCCGCTACCTGCTCC 780
Db	721 AAGTATCCATGAGTGTGATGATGCGGCGGTGATACGCTTGTATCCGCTACCTGCTCC 780

1861 AGCCTCACAGGCGGGACAGGAAACAGGTGCGAGGGGAGGTCCAGTGTCTCCACCGCA 1920
1861 AGCCTCACAGGCGGGACAGGAAACAGGTGCGAGGGGAGGTCCAGTGTCTCCACCGCA 1920
1921 ACACAATCTTTCTGCGGACCTGCGTCAATGCGGTGTTGGAGTGTCTATCATGTGTC 1980
1921 ACACAATCTTTCTGCGGACCTGCGTCAATGCGGTGTTGGAGTGTCTATCATGTGTC 1980
1981 GGTCTAAAGACCTTGTCCGGCCCAAGGCGCCAAATCACCCAAATGTACCAATGTGGAC 2040
1981 GGTCTAAAGACCTTGTCCGGCCCAAGGCGCCAAATCACCCAAATGTACCAATGTGGAC 2040
2041 CAGGACCTCGTGGGTGCGCAAGCGCCCGCGGGCGGTCTCTTGACACCATGCACTGC 2100
2041 CAGGACCTCGTGGGTGCGCAAGCGCCCGCGGGCGGTCTCTTGACACCATGCACTGC 2100
2101 GGCAGCTCGGACCTTTACTTGGTCAGAGGCGATGCGGATGCTATTCGGGTGCGCGCGG 2160
2101 GGCAGCTCGGACCTTTACTTGGTCAGAGGCGATGCGGATGCTATTCGGGTGCGCGCGG 2160
2161 GGCAGCAGCAGGGGAGGCTACTCTCTCCCGCAGGCGCGTCTCTTACTTGAAGGCTCTTCG 2220
2161 GGCAGCAGCAGGGGAGGCTACTCTCTCCCGCAGGCGCGTCTCTTACTTGAAGGCTCTTCG 2220
2221 GGCAGTCCACTGCTCTGCGGCTGCGGCGACGCTGTGGGCACTTTGCGGCTGCGCGGTGC 2280
2221 GGCAGTCCACTGCTCTGCGGCTGCGGCGACGCTGTGGGCACTTTGCGGCTGCGCGGTGC 2280
2281 ACCCGAGGGGTTCGAAGCGGTGAGCTTTGTACCGTCCGATGCTATGGAACCACTATG 2340
2281 ACCCGAGGGGTTCGAAGCGGTGAGCTTTGTACCGTCCGATGCTATGGAACCACTATG 2340
2341 CGGTCCCGGTCTTACAGGCAACTCGTCCCGCGCGGTACCGAGACATTTCCAGGTG 2400
2341 CGGTCCCGGTCTTACAGGCAACTCGTCCCGCGCGGTACCGAGACATTTCCAGGTG 2400
2401 GCCCATCTACAGGCGGCTTACTGTTAGCGGCAAGAGCACTAAGGTCCCGCTGCGTATGCA 2460
2401 GCCCATCTACAGGCGGCTTACTGTTAGCGGCAAGAGCACTAAGGTCCCGCTGCGTATGCA 2460
2461 GCCCAAGGGTATAGGTGCTTGTCTGAACCGCTCGGCGCGCACCTAGTTCGGG 2520
2461 GCCCAAGGGTATAGGTGCTTGTCTGAACCGCTCGGCGCGCACCTAGTTCGGG 2520
2521 GCGTATATGTTAAGGCACATGTTATGACCTTAACTAATCAGAACCGGGTAAAGACCATC 2580
2521 GCGTATATGTTAAGGCACATGTTATGACCTTAACTAATCAGAACCGGGTAAAGACCATC 2580
2581 ACCAGGGTCCCGCATCAGCTACTCCACCTATGCGCAACCGGGTAAAGACCATC 2640
2581 ACCAGGGTCCCGCATCAGCTACTCCACCTATGCGCAACCGGGTAAAGACCATC 2640
2641 TCTGGGGCGGCTATGACATCATATATGTGATGATGCGCACTCACTGACTGACCACT 2700
2641 TCTGGGGCGGCTATGACATCATATATGTGATGATGCGCACTCACTGACTGACCACT 2700
2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGCGGTGAGCGCGACTCGTCTGT 2760
2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGCGGTGAGCGCGACTCGTCTGT 2760
2761 CTGCGCACCGCTAGCGCTCGGGATCGGTACCGTGGCCACATCAAAATCGAGGAGGTG 2820
2761 CTGCGCACCGCTAGCGCTCGGGATCGGTACCGTGGCCACATCAAAATCGAGGAGGTG 2820
2821 GCTGTCTCAGCATGAGAAATCCCTTTTATGGCAAGCGCATCCCATCGAGACCATC 2880
2821 GCTGTCTCAGCATGAGAAATCCCTTTTATGGCAAGCGCATCCCATCGAGACCATC 2880
2881 AAGGGGGGAGGACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGCTCGCGCG 2940
2881 AAGGGGGGAGGACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGCTCGCGCG 2940
2941 AAGCTGTCCGGCTCGGACCAATGTGTAGCATATTTACCGGGGCTTGTATGATCGGTC 3000

2941 AAGCTGTCCGGCTCGGACCAATGTGTAGCATATTTACCGGGGCTTGTATGATCGGTC 3000
3001 ATACCAACTAGCGGAGACGTCATTGTCTGAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060
3001 ATACCAACTAGCGGAGACGTCATTGTCTGAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060
3061 GCGGATTTGCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
3061 GCGGATTTGCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
3121 CTGGACCCGACCTTACCACTTGAAGCGACGCGTCCCAAGAGCGGCTGACCGCTCG 3180
3121 CTGGACCCGACCTTACCACTTGAAGCGACGCGTCCCAAGAGCGGCTGACCGCTCG 3180
3181 CAGCGCGAGGAGGAGCTAGTGGGCGAGGATGGGCAITTTACAGGTTTGTGATCCAGGA 3240
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3241 GAACGGCCCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACCGGCTGT 3300
3241 GAACGGCCCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACCGGCTGT 3300
3301 GCTTGTGACAGCTCACGCGCGCGGAGACCTCAGTTAGGTTTGGGAGAGCTTTTAAACACA 3360
3301 GCTTGTGACAGCTCACGCGCGCGGAGACCTCAGTTAGGTTTGGGAGAGCTTTTAAACACA 3360
3361 CCAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTTC 3420
3361 CCAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTTC 3420
3421 ACCCATAGAGCGCCCATTTCTTGTCCAGACTAAGAGGCGAGAGCAACTTCCCTTAC 3480
3421 ACCCATAGAGCGCCCATTTCTTGTCCAGACTAAGAGGCGAGAGCAACTTCCCTTAC 3480
3481 CTGTGTAGCATACAGGCTACGCTGCGCGGCTCAGGCTCAGGCTCAGCTTCCATCTGGGAC 3540
3481 CTGTGTAGCATACAGGCTACGCTGCGCGGCTCAGGCTCAGGCTCAGCTTCCATCTGGGAC 3540
3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACACGGGCGGCGGCTTCTGCTG 3600
3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACACGGGCGGCGGCTTCTGCTG 3600
3601 TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAAAATACATC 3660
3601 TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAAAATACATC 3660
3661 ATGGCATGCTATGCTGCGGTGACCTGAGGTCTGAGGCTGCTGAGGCTGCTGCTGAGGCGGA 3720
3661 ATGGCATGCTATGCTGCGGTGACCTGAGGTCTGAGGCTGCTGAGGCTGCTGCTGAGGCGGA 3720
3721 GTCCTAGAGCTTGGCGCGGTATTTGCTGACACAGGAGCGTGGTCAITTTGCGGCGAGG 3780
3721 GTCCTAGAGCTTGGCGCGGTATTTGCTGACACAGGAGCGTGGTCAITTTGCGGCGAGG 3780
3781 ATCATCTTGTCCGAAAGCGGCGCATATTCCCGAGAGGGAAGTCTTTTACCGGAGTTC 3840
3781 ATCATCTTGTCCGAAAGCGGCGCATATTCCCGAGAGGGAAGTCTTTTACCGGAGTTC 3840
3841 GATGAGATGGAAGTGCCTCAGCTTCCCTTACATCGAAGGGAATGCACTGCTGCC 3900
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3901 GAACAATTTAAACAGAGGCAATCGGGTGTCTGCAACAGCCACCAAGAGGAGGCT 3960
3901 GAACAATTTAAACAGAGGCAATCGGGTGTCTGCAACAGCCACCAAGAGGAGGCT 3960
3961 GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGGGAGGAGCATATG 4020
3961 GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGGGAGGAGCATATG 4020
4021 TGGAAATTTATCAGCGGATACATATTTAGAGGCTTGTCCACTCTGCTGCTGGGAGCCCTC 4080

Db	4021	TGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGCTTGTCCACTCTCGCTGGCAACCCC	4080	Qy	5161	ACATTTCTGGTTCGGGCTCAATCAATACCTGGTGGTGCACAGCTCCCATGGAGCCCGAA	5220
Qy	4081	GGATAGCATCACTGATGGCAITTCACAGCTCTATCACAGCCCGCTCACCACCAACAT	4140	Db	5161	ACATTTCTGGTTCGGGCTCAATCAATACCTGGTGGTGCACAGCTCCCATGGAGCCCGAA	5220
Db	4081	GCATAGCATCACTGATGGCAITTCACAGCTCTATCACAGCCCGCTCACCACCAACAT	4140	Qy	5221	CCGAGCTAGCAGTGTCTCATTTCCATGCTCACCGACCCCTCCCAATTAACGGCGGAGACG	5280
Qy	4141	ACCTCTCTGTTTAACTATCCTGGGGGATGGTGGCGCCGCAACTTGTCTCTCCAGCGCT	4200	Db	5221	CCGAGCTAGCAGTGTCTCATTTCCATGCTCACCGACCCCTCCCAATTAACGGCGGAGACG	5280
Db	4141	ACCTCTCTGTTTAACTATCCTGGGGGATGGTGGCGCCGCAACTTGTCTCTCCAGCGCT	4200	Qy	5281	GCTAAGCGTATAGGCTGGCCAGGGGATCTCCCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
Qy	4201	GCTTCTGCTTTCGTAGCGCGCGGATCGCTGGAGCGGCTTGTGGCAGCATAGGCGCTTGG	4260	Db	5281	GCTAAGCGTATAGGCTGGCCAGGGGATCTCCCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
Db	4201	GCTTCTGCTTTCGTAGCGCGCGGATCGCTGGAGCGGCTTGTGGCAGCATAGGCGCTTGG	4260	Qy	5341	CTGCTCGCGCTTCTTGAAGGCAACATGACATACCTCCCTGATGATCTCCCGGACGCTGAC	5400
Qy	4261	AAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGCC	4320	Db	5341	CTGCTCGCGCTTCTTGAAGGCAACATGACATACCTCCCTGATGATCTCCCGGACGCTGAC	5400
Db	4261	AAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGCC	4320	Qy	5401	CTCATCGAGGCCAACCTCTCTGTCGGCGAGAGATGGCGGGAACATCACCCGCTGGAG	5460
Qy	4321	TTTAAAGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTTACTTCCCTGCT	4380	Db	5401	CTCATCGAGGCCAACCTCTCTGTCGGCGAGAGATGGCGGGAACATCACCCGCTGGAG	5460
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Qy	4381	ATCCTCTCCCTGCGCGCTAGTCTGCGGGTCTGTGCGCAGCGATPACTGCGTCGGCAC	4440	Db	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAGCGGAGGATGAG	5520
Db	4381	ATCCTCTCCCTGCGCGCTAGTCTGCGGGTCTGTGCGCAGCGATPACTGCGTCGGCAC	4440	Qy	5521	AGGGAAGTATCCGCTTCGCGGAGATCCTGCGAGGTCCAGGAAATTCCTTCGAGCGATG	5580
Qy	4441	GTGGGCCACAGGGAGGGGGCTGTGCACTGGATGAACCGGCTGATAGGTTTCGCTTCGGG	4500	Db	5521	AGGGAAGTATCCGCTTCGCGGAGATCCTGCGGAGGTCCAGGAAATTCCTTCGAGCGATG	5580
Db	4441	GTGGGCCACAGGGAGGGGGCTGTGCACTGGATGAACCGGCTGATAGGTTTCGCTTCGGG	4500	Qy	5581	CCCATATGGGCAACCGCGGATTAACAACCTCCACTGTAGAGTCTCGGAAGACCCCGAC	5640
Qy	4501	GGTAACACAGCTCTCCCAACGCTATGTGCTGAGAGCGAGCTGACAGCAGTGTCACT	4560	Db	5581	CCCATATGGGCAACCGCGGATTAACAACCTCCACTGTAGAGTCTCGGAAGACCCCGAC	5640
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Qy	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGGCTTCAACAGTGGATCAAC	4620	Db	5641	TACGCTCCCTCAGTGTGACACGGGTGTCATGTCGCTGCAAGGCGCTTCGATACCA	5700
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Qy	4621	GAGGACTGCTCAGCCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680	Db	5701	CCTCCACGAGGAGAGGACGGTGTGCTGTGACAGATCTACCGTGTCTTCTGCTTGGCG	5760
Db	4621	GAGGACTGCTCAGCCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680	Qy	5761	GAGCTCGCACAAAGACCTTCGGCAGCTCCGAATCGTGGCGCTCGACAGCGGCGACCGCA	5820
Qy	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAGTCCAGCTCTCCCGGGA	4740	Db	5761	GAGCTCGCACAAAGACCTTCGGCAGCTCCGAATCGTGGCGCTCGACAGCGGCGACCGCA	5820
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RESULT 11
AAA98968
ID AAA98968 standard; DNA; 7989 BP.
XX
AC AAA98968;
XX
DT 08-FEB-2001 (first entry)
XX
DE Hepatitis C virus DNA fragment SEQ ID NO: 4.
XX
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX
OS Hepatitis C virus.
XX
FN DE19915178-AL.
XX
PD 05-OCT-2000.
XX
PF 03-APR-1999; 99DE-01015178.
XX
PR 03-APR-1999; 99DE-01015178.
XX
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Bartschschlager R;

XX	WPI; 2000-629140/61.
XX	Cell culture system for hepatitis C virus, useful e.g. in screening for
XX	therapeutic agents, comprises human hepatoma cells containing a viral RNA
PT	construct that includes a selectable gene.
PT	
XX	Claim 8; Page 37-43; 58pp; German.
PS	
XX	This invention describes a novel Hepatitis C virus (HCV) cell culture
CC	system comprising human hepatoma cells that contain an integrated HCV-RNA
CC	construct (I). (I) contains the HCV-specific RNA segments 5'-NTR (non-
CC	translated region), NS (non-structural)3, NS4A, NS4B, NS5A, NS5B and 3'-
CC	NTR, and a selectable (marker) gene (II). The cell cultures, and/or (I),
CC	are used to prepare, evaluate and/or test therapeutic and/or diagnostic
CC	agents for HCV infections, and to prepare vaccines against HCV infection
CC	(particularly preparation of attenuated HCV). The can also be used for
CC	preparation of a liver-specific delivery system for gene therapy, and to
CC	identify cells permissive for HCV replication. Virus RNA replicates
CC	autonomously and with high efficiency in this cellular system, so that
CC	variations in replication rates can be measured (for screening antiviral
CC	agents) quantitatively or qualitatively, using standard laboratory
CC	equipment. Efficient replication of HCV RNA is only achieved when the
CC	specified RNA segments are present and when the transfected cells are
CC	maintained under permanent selection pressure
XX	
SQ	Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;
Query Match 100.0%; Score 7989; DB 3; Length 7989;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Dy	1 GCCAGCCCCGATTGGGGGCACACTCCACCATAGTCACTCCCTGTGAGGAATACTAGTG 60
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Qy	121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGGAACCGGTGAGTACACCGGAATTCGCCAG 180
Dy	121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGGAACCGGTGAGTACACCGGAATTCGCCAG 180
Qy	181 GACGACCGGGTCCTTTCTTTGGATCAACCCGCTCAATGCTGGAGATTTGGCGTGCCCCC 240
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Dy	241 CGGAGACTGCTAGCCGAGTAGTGTGGTTCGGGAAGGCTTGTGCTACTGCTCATAGG 300
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XX WO2004015131-A2.
XX 19-FEB-2004.
XX 12-AUG-2003; 2003WO-US025260.
XX 12-AUG-2002; 2002US-0402661P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Gao M, Lemm JA, O'boyle DR, Nower P, Rigat K, Sun J;
XX WPI; 2004-180685/17.
XX P-PSDB; ADJ57846.
XX Use of hepatitis C virus assays or reporter assays, e.g. identifying a
XX compound that inhibits hepatitis C virus RNA replication or identifying a
XX compound that modulates the activity of a gene of interest.
XX PS
XX Claim 3; SEQ ID NO 1; 45pp; English.
XX
XX The present invention relates to the use of hepatitis C virus (HCV)
XX assays for identifying a compound that inhibits HCV RNA replication and
XX reporter assays for identifying a compound that modulates the activity of
XX a gene of interest. The assays are useful for identifying a compound that
XX inhibits HCV RNA replication or for identifying a compound that modulates
XX the activity of a gene of interest. The HCV assay is useful for high
XX throughput screening that quantifies both the amount of HCV RNA
XX replication inhibitory activity associated with a test compound and the
XX amount of cytotoxicity associated with the test compound. The compound is
XX useful for treating hepatitis C infection. Assays of the invention have
XX distinct advantages when compared to qRT-PCR or other methods in that
XX assays of the invention may take place in situ in a detergent based crude
XX cell lysate, which requires no further preparation prior to performing
XX the assays. The assays do not also involve numerous manipulations to add
XX or subtract reagents after addition of test compounds and are desirably
XX based on a viral protein which is required by the HCV replicon for
XX replication. The present sequence represents a HCV replicon encoding
XX sequence used in the assay of the invention.
XX
XX Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;
Query Match 100.0%; Score 7989; DB 12; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAACACTGTG 60
DB 1 GCCAGCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAACACTGTG 60
QY 61 TCTTCACGACGAAACGGCTAGCCATGGCGTTAGTATGATGTCGTGAGCCCTCCAGGAC 120
DB 61 TCTTCACGACGAAACGGCTAGCCATGGCGTTAGTATGATGTCGTGAGCCCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB 121 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
QY 181 GACGACCGGTCTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGGTGCCCCC 240
DB 181 GACGACCGGTCTCTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGGTGCCCCC 240
QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGG 300
DB 241 GCGAGACTCTAGCCGAGTAGTGTGGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGG 300
QY 301 GTGCTTGCGAGTGCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTGCGAGTGCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360

DB 301 GTGCTTGCGAGTGCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAAGAGAAAACCAAGGGCGGCCCATGATTGAACAGATGAGATTGCACGACGTTCTC 420
DB 361 CTCAAGAGAAAACCAAGGGCGGCCCATGATTGAACAGATGAGATTGCACGACGTTCTC 420
QY 421 CGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
DB 421 CGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGACAATCGGCTGCT 480
QY 481 CTGATGCGCGCGTGTTCGGCTGTGAGCGAGGGGCGCCGGTCTTTTTCAGACCG 540
DB 481 CTGATGCGCGCGTGTTCGGCTGTGAGCGAGGGGCGCCGGTCTTTTTCAGACCG 540
QY 541 ACCTGTCCGGTGCCTGAATGAACCTGAGGACGAGGACGCGGCTATCTGTGGTGGCCA 600
DB 541 ACCTGTCCGGTGCCTGAATGAACCTGAGGACGAGGACGCGGCTATCTGTGGTGGCCA 600
QY 601 CGACGGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC 660
DB 601 CGACGGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC 660
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DB 661 TGCTATTGGGCGAAGTGCAGGAGGAGGATCTCTGTCACTCACTCTCTCTCTCCGAGA 720
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DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGTACTCTGCC 780
QY 781 CATTGACACCAAGCGAACAATCGATCGAGGACGACTACTCGGATGGAAGCGGTC 840
DB 781 CATTGACACCAAGCGAACAATCGATCGAGGACGACTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGATGATCTGACGAGAGATCAGGGCTCGCGCAGCGCACTGCTTCG 900
DB 841 TTGTGATCAGATGATCTGACGAGAGATCAGGGCTCGCGCAGCGCACTGCTTCG 900
QY 901 CCAGCTCAAGCGCGCATGCTCCGACGCGAGGATCTCGTGTGACCATCGCGATGCT 960
DB 901 CCAGCTCAAGCGCGCATGCTCCGACGCGAGGATCTCGTGTGACCATCGCGATGCT 960
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DB 1021 TGGGTGCGCGGACCGCTATCAGGACATAGCGTGGCTACCGCTGATATTGCTGAAGAC 1080
QY 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
DB 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
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DB 1141 AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
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DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTACTGGC 1260
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DB 1261 CGAAGCCGCTTGAATAAGCGGCTGTGGTGTGTATATGTTATTTCCACCATATTG 1320
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DB 1321 CGGTCTTTTGGCAATGTGAGGCGCCGGAACCTGCGCCCTGTCTTCTGACGAGCAATCCT 1380
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DB 1381 AGGGGTCTTTCCTCTCTCGCAAGAAATGCAAGTCTGTTGAATGTGCTGAAGGAAGA 1440

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2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAAAGCCATCCCATCGAGACCATC 2880
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3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTAAGCTGATGATGATGATGATGATGATGATG 3600
3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTAAGCTGATGATGATGATGATGATGATGATG 3600
3601 TATAGGCTGGAGCGGCTTCAAAACGAGGTTACTACCACACACCCCAATACCAATATACATC 3660

Db	3601	TATAGCTGGAGCCGTTCAAAACGAGTTACTACACACACCCCATACCAATACATC	3660	Db	4681	ACGGTGTGATGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATTTGCCGGGA	4740
Qy	3661	ATGGCATGATGTCGGCTGACCTGGAGGTCGTCAACGAGCACTGGGTGCTGGTAGCGGA	3720	Qy	4741	GTCCCTCTTCTTCATGTCAAAGTGGGTACAAGAGAGTCTGGCGGGCGACAGCATCATG	4800
Db	3661	ATGGCATGATGTCGGCTGACCTGGAGGTCGTCAACGAGCACTGGGTGCTGGTAGCGGA	3720	Db	4741	GTCCCTCTTCTTCATGTCAAAGTGGGTACAAGAGAGTCTGGCGGGCGACAGCATCATG	4800
Qy	3721	GTCTAGCAGCTCTGGCCCGGTATGCTGACACAGGAGCGTGGTCAATGTTGGGCAGG	3780	Qy	4801	CAAAACACCTGCCCATGTGGAGCACAGATCAACGGACATGTGAAAAACGGTTCATAGG	4860
Db	3721	GTCTAGCAGCTCTGGCCCGGTATGCTGACACAGGAGCGTGGTCAATGTTGGGCAGG	3780	Db	4801	CAAAACACCTGCCCATGTGGAGCACAGATCAACGGACATGTGAAAAACGGTTCATAGG	4860
Qy	3781	ATCATCTTGTCCGAAAGCCGGCCATCATTTCCGACAGGGAAGTCTTTTACCCGGAGTTC	3840	Qy	4861	ATCGTGGGGCTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGGCTAC	4920
Db	3781	ATCATCTTGTCCGAAAGCCGGCCATCATTTCCGACAGGGAAGTCTTTTACCCGGAGTTC	3840	Db	4861	ATCGTGGGGCTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGGCTAC	4920
Qy	3841	GATGAGTAGAAGTGGCTTACACCTCCCTTACATCGAACAGGGAATGCAAGCTCGCC	3900	Qy	4921	ACCACGGGCCCTGCACGCCCTCCCGGCCCAAAATTAATTTCTAGGGCGCTGTGCGGGTG	4980
Db	3841	GATGAGTAGAAGTGGCTTACACCTCCCTTACATCGAACAGGGAATGCAAGCTCGCC	3900	Db	4921	ACCACGGGCCCTGCACGCCCTCCCGGCCCAAAATTAATTTCTAGGGCGCTGTGCGGGTG	4980
Qy	3901	GAACAAATTCAGAGAGCAATCGGGTTGCTGCAACAGCCAGCAAGCAAGCGGAGCT	3960	Qy	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGATG	5040
Db	3901	GAACAAATTCAGAGAGCAATCGGGTTGCTGCAACAGCCAGCAAGCAAGCGGAGCT	3960	Db	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGATG	5040
Qy	3961	GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	Qy	5041	ACCACTACAAACGTAAAGTCCCGTGTACAGTTCGGGCCCGCCCGAATTTCTTACAGAAAGTG	5100
Db	3961	GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	Db	5041	ACCACTACAAACGTAAAGTCCCGTGTACAGTTCGGGCCCGCCCGAATTTCTTACAGAAAGTG	5100
Qy	4021	TGGAAATTCATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTGCCTGGCAACCCC	4080	Qy	5101	GATGGGTGCGGTGACAGCTACGCTCCAGCGTGCAAAACCCCTCTTACCGGAGGAGTGC	5160
Db	4021	TGGAAATTCATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTGCCTGGCAACCCC	4080	Db	5101	GATGGGTGCGGTGACAGCTACGCTCCAGCGTGCAAAACCCCTCTTACCGGAGGAGTGC	5160
Qy	4081	GCGATAGCATCAGTGGGATTCACAGCTCTATCACCAGCCGCTTCAACCCCAACAT	4140	Qy	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGCGAGCCCGAA	5220
Db	4081	GCGATAGCATCAGTGGGATTCACAGCTCTATCACCAGCCGCTTCAACCCCAACAT	4140	Db	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGCGAGCCCGAA	5220
Qy	4141	ACCTCTCTGTTTAAATCCTCGGGGAGTGGGTGGCGCCGCAACTTGTCTCCAGCGCT	4200	Qy	5221	CCGACGTAGAGTGTCTTCCATGCTCAACGACCCCTCCACATTTAGCGCGAGACG	5280
Db	4141	ACCTCTCTGTTTAAATCCTCGGGGAGTGGGTGGCGCCGCAACTTGTCTCCAGCGCT	4200	Db	5221	CCGACGTAGAGTGTCTTCCATGCTCAACGACCCCTCCACATTTAGCGCGAGACG	5280
Qy	4201	GCTTCTGCTTTCGATAGGCGCGGATCGCTGGAGGGTGTGGCAGATAGGCTTGGG	4260	Qy	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340
Db	4201	GCTTCTGCTTTCGATAGGCGCGGATCGCTGGAGGGTGTGGCAGATAGGCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340
Qy	4261	AAGTGTCTTGGGATATTTGCGAGTTATGAGCAGGGGTGAGAGGGGCTGTGGCC	4320	Qy	5341	CTGTCTGGGCTTCTTTGAAAGCAACATGACCTACCGTCTATGACTCCCGGAGCGCTGAC	5400
Db	4261	AAGTGTCTTGGGATATTTGCGAGTTATGAGCAGGGGTGAGAGGGGCTGTGGCC	4320	Db	5341	CTGTCTGGGCTTCTTTGAAAGCAACATGACCTACCGTCTATGACTCCCGGAGCGCTGAC	5400
Qy	4321	TTTAAGGTCTATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCT	4380	Qy	5401	CTCATCGAGGCAACCTCTCTGTGGCGGAGAGATGGCGGGAAACATCACCGCGTGGAG	5460
Db	4321	TTTAAGGTCTATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCT	4380	Db	5401	CTCATCGAGGCAACCTCTCTGTGGCGGAGAGATGGCGGGAAACATCACCGCGTGGAG	5460
Qy	4381	ATCCTCTCCCTGGGCCCTAGTGTGGGTGCTGAGAGGCTGGTAACTACTCCCTGCT	4440	Qy	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCAGAGCGCTCCAAAGCGGAGGAGATGAG	5520
Db	4381	ATCCTCTCCCTGGGCCCTAGTGTGGGTGCTGAGAGGCTGGTAACTACTCCCTGCT	4440	Db	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCAGAGCGCTCCAAAGCGGAGGAGATGAG	5520
Qy	4441	GTGGCCACAGGGAGGGGCTGTGAGTGAATGAACCGGCTGATAGCGCTTCCGCTGCGG	4500	Qy	5521	AGGAAAGTATCCGTTCCGCGGAGATCCTGCGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGCCACAGGGAGGGGCTGTGAGTGAATGAACCGGCTGATAGCGCTTCCGCTGCGG	4500	Db	5521	AGGAAAGTATCCGTTCCGCGGAGATCCTGCGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
Qy	4501	GGTAACCAAGTCTCCCGACGCACTATGTGCTGAGAGCGAGCGCTGACAGCTGTCACT	4560	Qy	5581	CCCATATGGGCACCGCGGATTTACAACCTCTCCACTGTGTAGAGTCTGTGAAAGGACCCGGAC	5640
Db	4501	GGTAACCAAGTCTCCCGACGCACTATGTGCTGAGAGCGAGCGCTGACAGCTGTCACT	4560	Db	5581	CCCATATGGGCACCGCGGATTTACAACCTCTCCACTGTGTAGAGTCTGTGAAAGGACCCGGAC	5640
Qy	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCAACAGTGGATCAAC	4620	Qy	5641	TACGTCCCTCAGTGGTACACGGGTGTCCATTTGCGCGCTGCAAGGGCCCTCCCATACCA	5700
Db	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCAACAGTGGATCAAC	4620	Db	5641	TACGTCCCTCAGTGGTACACGGGTGTCCATTTGCGCGCTGCAAGGGCCCTCCCATACCA	5700
Qy	4621	GAGGACTGTCTCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680	Qy	5701	GCTCCAGGAGGAGGACGGTGTCTGTGAGAACTTACCGTGTCTTCTGCTTGGCG	5760
Db	4621	GAGGACTGTCTCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680	Db	5701	GCTCCAGGAGGAGGACGGTGTCTGTGAGAACTTACCGTGTCTTCTGCTTGGCG	5760
Qy	4681	ACGGTGTGATGATTTTAAGACCTGGGCTCAGTCCAAAGCTCCTGCGCGGATTTGCGGGA	4740	Qy	5761	GAGCTCGGCAACAAAGACCTTCGGCAGCTCCGAACTGTCGGCGCTCGACAGCGGACGGA	5820
Db	4681	ACGGTGTGATGATTTTAAGACCTGGGCTCAGTCCAAAGCTCCTGCGCGGATTTGCGGGA	4740	Db	5761	GAGCTCGGCAACAAAGACCTTCGGCAGCTCCGAACTGTCGGCGCTCGACAGCGGACGGA	5820

QY	5821	ACGGCTCTCTCTGACCAAGCCCTTCGAGCAGCGCGACCGGGGATCCGAGTTCGAGTTGAGTCTGTAC	5880
DB	5821	ACGGCTCTCTCTGACCGAGCCCTTCGAGCAGCGCGACCGGGATCCGAGTTCGAGTTGAGTCTGTAC	5880
QY	5881	TCCTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCAGCGGTCCTTGG	5940
DB	5881	TCCTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCAGCGGTCCTTGG	5940
QY	5941	TCTACCGTAAGCGAGGAGCTAGTGAAGACGTCTCTCTGCTGTCTGATCTCAGACCTCAACATGG	6000
DB	5941	TCTACCGTAAGCGAGGAGCTAGTGAAGACGTCTCTCTGCTGTCTGATCTCAGACCTCAACATGG	6000
QY	6001	ACAGCGCCCTGATCAGCCATCGCTGCGGAGAGAAACGAGCTGCCCATCAATGCACTG	6060
DB	6001	ACAGCGCCCTGATCAGCCATCGCTGCGGAGAGAAACGAGCTGCCCATCAATGCACTG	6060
QY	6061	AGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTACAACTCTCGACGCGCAAGC	6120
DB	6061	AGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTACAACTCTCGACGCGCAAGC	6120
QY	6121	CTCGCGCAGAAAGGTCACTTTGACAGACTGCAAGTCTCTGACACCACTACCGGAC	6180
DB	6121	CTCGCGCAGAAAGGTCACTTTGACAGACTGCAAGTCTCTGACACCACTACCGGAC	6180
QY	6181	GTGCTCAAGAGATGAAGGCGAAGCGCTGCACAGTTAAGCTAACTTCTATCCGTGGAG	6240
DB	6181	GTGCTCAAGAGATGAAGGCGAAGCGCTGCACAGTTAAGCTAACTTCTATCCGTGGAG	6240
QY	6241	GAAGCTGTAACTGACGCCCCACATTCGCGCAGATCTAAATTTGGCTATGGGCGAAAG	6300
DB	6241	GAAGCTGTAACTGACGCCCCACATTCGCGCAGATCTAAATTTGGCTATGGGCGAAAG	6300
QY	6301	GACGTCGGAACTTATCAGGAAAGCGGTTAAACCAATCCGCTCGGTGGAAGACTTG	6360
DB	6301	GACGTCGGAACTTATCAGGAAAGCGGTTAAACCAATCCGCTCGGTGGAAGACTTG	6360
QY	6361	CTGGAAGACACTGAGACACCAATTTGACCAACCACTCATGGCAAAAATGAGGTTTCTGC	6420
DB	6361	CTGGAAGACACTGAGACACCAATTTGACCAACCACTCATGGCAAAAATGAGGTTTCTGC	6420
QY	6421	GTCCAAACGAGAGGGGGCCGCAAGCCAGCTCGCTTATCTGATTTCCAGATTTGGGG	6480
DB	6421	GTCCAAACGAGAGGGGGCCGCAAGCCAGCTCGCTTATCTGATTTCCAGATTTGGGG	6480
QY	6481	GTTCGTGTGCGAGAAAATGGCCCTTACAGATGTGGTCTCCACCTCCCTCAGGCCGTG	6540
DB	6481	GTTCGTGTGCGAGAAAATGGCCCTTACAGATGTGGTCTCCACCTCCCTCAGGCCGTG	6540
QY	6541	ATGGGCTCTTCATACGGATTCCAATCTCTCTGAGCAGCGGTCCAGTTCTCTGGTGAAT	6600
DB	6541	ATGGGCTCTTCATACGGATTCCAATCTCTCTGAGCAGCGGTCCAGTTCTCTGGTGAAT	6600
QY	6601	GCTTGGAACGCGAAGAAATCCCTATGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
DB	6601	GCTTGGAACGCGAAGAAATCCCTATGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
QY	6661	ACGCTCACTCAGATGACATCCGTGTGAGGATCAATCTAACATGTTGTACTTGGCC	6720
DB	6661	ACGCTCACTCAGATGACATCCGTGTGAGGATCAATCTAACATGTTGTACTTGGCC	6720
QY	6721	CCGGAAGCCAGACAGGCCATAAGGTCTCAGAGCGGCTTTACATCGGGGCCCCCTG	6780
DB	6721	CCGGAAGCCAGACAGGCCATAAGGTCTCAGAGCGGCTTTACATCGGGGCCCCCTG	6780
QY	6781	ACTAATTTCTAAAGGCGAAGCTCGGCTATFCGCGGTGCGCGCGAGCGGTCTACTGACG	6840
DB	6781	ACTAATTTCTAAAGGCGAAGCTCGGCTATFCGCGGTGCGCGCGAGCGGTCTACTGACG	6840
QY	6841	ACGAGCTCGCGTAAATACCTTCAATGTTACTTGAAGCGCGCTGCGGCTGTGAGCTGG	6900
DB	6841	ACGAGCTCGCGTAAATACCTTCAATGTTACTTGAAGCGCGCTGCGGCTGTGAGCTGG	6900

Qy	6901	AAGCTCCAGGACTCGACGATGCTCGTATGCGGAGACGACCTTGTGCTTATCTGTGAAAGC	6960
Db	6901	AAGCTCCAGGACTCGACGATGCTCGTATGCGGAGACGACCTTGTGCTTATCTGTGAAAGC	6960
Qy	6961	CGCGGGACCCAAAGAGGACGAGGCGAGCCTACGGGCTTACGAGGAGCTATGACTAGTATC	7020
Db	6961	CGCGGGACCCAAAGAGGACGAGGCGAGCCTACGGGCTTACGAGGAGCTATGACTAGTATC	7020
Qy	7021	TCTGCCCCCTCGGGGACCGCCCAACACAGAAATACGACTTGGAGTTGATTAACATCATGC	7080
Db	7021	TCTGCCCCCTCGGGGACCGCCCAACACAGAAATACGACTTGGAGTTGATTAACATCATGC	7080
Qy	7081	TCCTCCAAATGTTGAGTCGCGCAGATGCAATCTGGCAAAAGGCTGACTATCTCACCCGT	7140
Db	7081	TCCTCCAAATGTTGAGTCGCGCAGATGCAATCTGGCAAAAGGCTGACTATCTCACCCGT	7140
Qy	7141	GACCCACCAACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Db	7141	GACCCACCAACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Qy	7201	TCCTGGCTAGGCAACATCATCATGATATGCGCCACACTTGTGGCAAGGATGATCTGTATG	7260
Db	7201	TCCTGGCTAGGCAACATCATCATGATATGCGCCACACTTGTGGCAAGGATGATCTGTATG	7260
Qy	7261	ACTCATTTCTCTCCATPCCTTCAGTCTAGGAAACAACTTGA AAAAGCCCTAGATTGTCA	7320
Db	7261	ACTCATTTCTCTCCATPCCTTCAGTCTAGGAAACAACTTGA AAAAGCCCTAGATTGTCA	7320
Qy	7321	ATCTACGGGGCTGTACTCCATTGAGCCACTTGACTACCTCAGATCAATCAAGCACTC	7380
Db	7321	ATCTACGGGGCTGTACTCCATTGAGCCACTTGACTACCTCAGATCAATCAAGCACTC	7380
Qy	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Db	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Qy	7441	TCATGCTCAGGAAACTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGGGCCAGAACT	7500
Db	7441	TCATGCTCAGGAAACTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGGGCCAGAACT	7500
Qy	7501	GTCCGCGCTAGGCTACTGTCTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Db	7501	GTCCGCGCTAGGCTACTGTCTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Qy	7561	AACTGGGCAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGCTCGCTCCAGTTGGAT	7620
Db	7561	AACTGGGCAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGCTCGCTCCAGTTGGAT	7620
Qy	7621	TTATCCAGCTGGTTCGTGCTGTGTTACGCGGGGAGACATATATCACAGCTGTCTCGT	7680
Db	7621	TTATCCAGCTGGTTCGTGCTGTGTTACGCGGGGAGACATATATCACAGCTGTCTCGT	7680
Qy	7681	GCCCGACCCGCTGGTTCATGTGGTGCCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCCGACCCGCTGGTTCATGTGGTGCCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
Qy	7741	CTACTCCCAACCGATGAACGGGAGCTAAAACACTCCAGGCCAAATAGGCCATCTGTGTTT	7800
Db	7741	CTACTCCCAACCGATGAACGGGAGCTAAAACACTCCAGGCCAAATAGGCCATCTGTGTTT	7800
Qy	7801	TTTCCCTTTTTTTTTTCTT	7860
Db	7801	TTTCCCTTTTTTTTTTCTT	7860
Qy	7861	TTTTTCCTCTTTTTTTTCTTTTTTTCTTTTCTTTTGGTGCTCCATCTTAGGCCCTAGTCA	7920
Db	7861	TTTTTTCTCTTTTTTTTCTTTTTTTCTTTTCTTTTGGTGCTCCATCTTAGGCCCTAGTCA	7920
Qy	7921	TAGCTGTGAAGGTCCGTCAGCGCTTGACTCGAGAGATGCTGATCTGGCCTCTCTGC	7980
Db	7921	TAGCTGTGAAGGTCCGTCAGCGCTTGACTCGAGAGATGCTGATCTGGCCTCTCTGC	7980
Qy	7981	AGATCAAGT	7989


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Db      7981 AGATCAAGT 7989
|||||||
RESULT 13
ABK91440
ID   ABK91440 standard; DNA; 10690 BP.
XX
AC   ABK91440;
XX
DT   15-NOV-2002 (first entry)
XX
DE   Hepatitis C virus vector construct pHCVNeo.17m7.
XX
KW   HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW   hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW   internal ribosome entry site; IRES; NSSA; HCV replication; mutant.
XX
OS   Hepatitis C virus.
OS   Encephalomyocarditis virus.
OS   Escherichia coli.
OS   Enterobacteria phage T7.
OS   Synthetic.
XX
PH   Key
FT   5'UTR
FT   1..341
FT   /tag= a
FT   CDS
FT   342..1181
FT   /tag= b
FT   /product= "Core-neo fusion protein"
FT   1190..1800
FT   /tag= c
FT   /label= IRES
FT   /note= "Internal ribosome entry site from EMCV"
FT   1801..7758
FT   /tag= d
FT   /product= "Polyprotein"
FT   /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT   mutation
FT   replace(4847,A)
FT   /tag= e
FT   mutation
FT   replace(5243,C)
FT   /tag= f
FT   3'UTR
FT   7759..7991
FT   /tag= g
FT   misc_feature
FT   7992..10690
FT   /tag= h
FT   /note= "Plasmid derived sequences"
XX
PN   WO200259321-A2.
XX
PD   01-AUG-2002.
XX
XX   16-JAN-2002; 2002WO-EP000526.
XX
XX   23-JAN-2001; 2001US-0263479P.
XX
XX   (RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.
XX
XX   De Francesco R, Migliaccio G, Paonessa G;
XX   WPI; 2002-599793/64.
XX
XX   New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX   NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX   ribosome entry site (IRES) region, useful in studying HCV replication and
XX   expression.
XX
XX   Claim 16; Page; 69pp; English.
XX
XX   The invention relates to nucleic acid molecules comprising altered HCV
XX   NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX   internal ribosome entry site (IRES) region coding for one or more NS3,
XX   NSSA, or EMCV IRES mutations, respectively. The location of the mutations

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CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replication and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVNeo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in Claim 16
XX
SQ   Sequence 10690 BP; 2333 A; 3045 C; 2908 G; 2404 T; 0 U; 0 Other;
Query Match      100.0%; Score 7988.8; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY   1 GCCAGCCCCGATGGGGCGCACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
DB   1 GCCAGCCCCGATGGGGCGCACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
QY   61 TCTTACGCGAAGAGCTCTAGCCATGGCGTTAGTATGATGCTGTCAGCCTCCAGGAC 120
DB   61 TCTTACGCGAAGAGCTCTAGCCATGGCGTTAGTATGATGCTGTCAGCCTCCAGGAC 120
QY   121 CCCCTCCCGGAGAGCCATAGTGTCTCGGAACCGGTAGTACACCGGAATTGCCAG 180
DB   121 CCCCTCCCGGAGAGCCATAGTGTCTCGGAACCGGTAGTACACCGGAATTGCCAG 180
QY   181 GAGCACCAGGTCCTTTCTTGGATCAACCCGCTCAATGCTGAGATTGGCGGTGCC 240
DB   181 GAGCACCAGGTCCTTTCTTGGATCAACCCGCTCAATGCTGAGATTGGCGGTGCC 240
QY   241 GCGAGACTGTCAGCGAGTAGTGTGGTTCGGAAGCCCTTGTGCTACTGCTGATAGG 300
DB   241 GCGAGACTGTCAGCGAGTAGTGTGGTTCGGAAGCCCTTGTGCTACTGCTGATAGG 300
QY   301 GTGCTTCGAGTGCCCGGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
DB   301 GTGCTTCGAGTGCCCGGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
QY   361 CTCAGAGAAAACCAAGAGGCGGCCCATGATTGAACAAGATGGATTGCACGAGTTCTC 420
DB   361 CTCAGAGAAAACCAAGAGGCGGCCCATGATTGAACAAGATGGATTGCACGAGTTCTC 420
QY   421 CGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGATGGGCAACACAGACATCGCTGCT 480
DB   421 CGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGATGGGCAACACAGACATCGCTGCT 480
QY   481 CTGATGCGCGCTGTCGGCTGTCAGCGAGGCGGCCGCTTCTTTTCTCAAGACCG 540
DB   481 CTGATGCGCGCTGTCGGCTGTCAGCGAGGCGGCCGCTTCTTTTCTCAAGACCG 540
QY   541 ACCTGTCCGCTGCTGAATGAATGACAGGAGGCGAGCGCGCTATTCGTGGTGGCCA 600
DB   541 ACCTGTCCGCTGCTGAATGAATGACAGGAGGCGAGCGCGCTATTCGTGGTGGCCA 600
QY   601 CGACGGCGTTCCTTGGCAGCTGCTGTCAGCTTGTCACTGAAGCGGAGGAGGACTGGC 660
DB   601 CGACGGCGTTCCTTGGCAGCTGCTGTCAGCTTGTCACTGAAGCGGAGGAGGACTGGC 660
QY   661 TGCTATTGGGCGAAGTGCCGGGCGAGGATCTCTCTATCTACCTTCTCTGCGCGAGA 720
DB   661 TGCTATTGGGCGAAGTGCCGGGCGAGGATCTCTCTATCTACCTTCTCTGCGCGAGA 720

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QY 721 AAGTATCCATCATGGCTGATGCAATCGCGCGCTGCATACGCTTGATCGGCTACCTGCC 780
DB 721 AAGTATCCATCATGGCTGATGCAATCGCGCGCTGCATACGCTTGATCGGCTACCTGCC 780
QY 781 CATTCGACCAACAGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCC 840
DB 781 CATTCGACCAACAGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCC 840
QY 841 TTGTGATCAGGATGATCTGAGCAGAGAGCATCAGGGGCTCGCGCGAGCGAAGCTCTTTCG 900
DB 841 TTGTGATCAGGATGATCTGAGCAGAGAGCATCAGGGGCTCGCGCGAGCGAAGCTCTTTCG 900
QY 901 CAGGCTCAAGCGCGCATGCGCGAGAGATCTCGTGTGACCCATGCGATGCGCT 960
DB 901 CAGGCTCAAGCGCGCATGCGCGAGAGATCTCGTGTGACCCATGCGATGCGCT 960
QY 961 GCTTCGGAATATCATGTTGGAATATGCGGCTTTCTGATTCATCGATTCGATTCG 1020
DB 961 GCTTCGGAATATCATGTTGGAATATGCGGCTTTCTGATTCATCGATTCGATTCG 1020
QY 1021 TGCGTGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGAAGAGC 1080
DB 1021 TGCGTGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGCGCTGACCGCTTCTCGTGTGATTCGATTCGATTCGATTCG 1140
DB 1081 TTGGCGGGAATGCGCTGACCGCTTCTCGTGTGATTCGATTCGATTCGATTCG 1140
QY 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTAAACAGACCAACG 1200
DB 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTAAACAGACCAACG 1200
QY 1201 GTTCCCTCTAGCGGATCAATTCGCGCCCTCTCGCTCCCCCCCCCTAACCTTACTGCG 1260
DB 1201 GTTCCCTCTAGCGGATCAATTCGCGCCCTCTCGCTCCCCCCCCCTAACCTTACTGCG 1260
QY 1261 CGAAGCGCTTGAATAGCGCGTGTGCGTTTGTCTATATGTTATTTTCAACCATATTG 1320
DB 1261 CGAAGCGCTTGAATAGCGCGTGTGCGTTTGTCTATATGTTATTTTCAACCATATTG 1320
QY 1321 CCGTCTTTTGGCAATGTCAGGCGCCGGAACCTGCGCCCTGCTTCTTACGAGCATTCCT 1380
DB 1321 CCGTCTTTTGGCAATGTCAGGCGCCGGAACCTGCGCCCTGCTTCTTACGAGCATTCCT 1380
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGAAAGGAACA 1440
DB 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGAAAGGAACA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTAGGACCCCTTTGAGGACGGG 1500
DB 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTAGGACCCCTTTGAGGACGGG 1500
QY 1501 AACCCCGCACCTGCGCAGAGTGCCTCTGCGGCCAAAGCCACGCTGATAGATACACCT 1560
DB 1501 AACCCCGCACCTGCGCAGAGTGCCTCTGCGGCCAAAGCCACGCTGATAGATACACCT 1560
QY 1561 GCAAAGCGGCAACCCAGTGCACGTTGTGAGTTGGATGTTGTGAAAGAGTCAAA 1620
DB 1561 GCAAAGCGGCAACCCAGTGCACGTTGTGAGTTGGATGTTGTGAAAGAGTCAAA 1620
QY 1621 TGCTCTCTCAAGCTATTCAACAAGGGCTGAAGGATGCCAAGAGGTACCCCAATTGT 1680
DB 1621 TGCTCTCTCAAGCTATTCAACAAGGGCTGAAGGATGCCAAGAGGTACCCCAATTGT 1680
QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCAAGGTTAAA 1740
DB 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCAAGGTTAAA 1740
QY 1741 AACGTCTAGGCGCCCGGAAACCAAGGCGAGTGTGTTTCTTTTGAAGAACGATATACC 1800
DB 1741 AACGTCTAGGCGCCCGGAAACCAAGGCGAGTGTGTTTCTTTTGAAGAACGATATACC 1800
QY 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCACT 1860

DB 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCACT 1860
QY 1861 AGCCTCACAGGCGGACAGGAACACAGGTGAGGGGGAGGTCCAAAGTGTCTCCACGCA 1920
DB 1861 AGCCTCACAGGCGGACAGGAACACAGGTGAGGGGGAGGTCCAAAGTGTCTCCACGCA 1920
QY 1921 ACACATCTTTCTGGCGACCTGCGTCAATGCGGTGTGTGGACTGTCTATCATGTGTC 1980
DB 1921 ACACATCTTTCTGGCGACCTGCGTCAATGCGGTGTGTGGACTGTCTATCATGTGTC 1980
QY 1981 GGTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCAAAATGTACCAATGTGGAC 2040
DB 1981 GGTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCAAAATGTACCAATGTGGAC 2040
QY 2041 CAGGACCTGTCGCTGCGTCAAGCGCCCCCGGGGCGCTTCTTGCACATGCACCTGC 2100
DB 2041 CAGGACCTGTCGCTGCGTCAAGCGCCCCCGGGGCGCTTCTTGCACATGCACCTGC 2100
QY 2101 GCGAGCTCGACCTTACTTGTGTCAGAGGCATGCGGATGTCAATTCGGTGTGCGCGG 2160
DB 2101 GCGAGCTCGACCTTACTTGTGTCAGAGGCATGCGGATGTCAATTCGGTGTGCGCGG 2160
QY 2161 GCGGACAGCAGGGGAGCGCTACTCTCCCCAGGCGCGCTTCTTGCACATGCACCTGC 2220
DB 2161 GCGGACAGCAGGGGAGCGCTACTCTCCCCAGGCGCGCTTCTTGCACATGCACCTGC 2220
QY 2221 GCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTGGGCTGCGGTGTC 2280
DB 2221 GCGGTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTCGAGGCGGTGACTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
DB 2281 ACCGAGGGGTTCGAGGCGGTGACTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
QY 2341 CCGTCCCCCGTCTTCAAGCAAACTCGCTCCCTCGGCGGTACCGACACATTCAGGTG 2400
DB 2341 CCGTCCCCCGTCTTCAAGCAAACTCGCTCCCTCGGCGGTACCGACACATTCAGGTG 2400
QY 2401 GCGCATPACACGCGCTTACTGTTAGCGGCAAGAGCACTAAGGTGCGGTATGCA 2460
DB 2401 GCGCATPACACGCGCTTACTGTTAGCGGCAAGAGCACTAAGGTGCGGTATGCA 2460
QY 2461 GCGCAAGGTATAGGTGCTTGTCTGAACCGCTCGTGCAGCACCTAGTTTTCGG 2520
DB 2461 GCGCAAGGTATAGGTGCTTGTCTGAACCGCTCGTGCAGCACCTAGTTTTCGG 2520
QY 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC 2580
DB 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC 2580
QY 2581 ACCAGGGTCCCCCATCAAGTACTCCACCTATGCGCAAGTTTCTTGGCGAGTGTG 2640
DB 2581 ACCAGGGTCCCCCATCAAGTACTCCACCTATGCGCAAGTTTCTTGGCGAGTGTG 2640
QY 2641 TCTGGGCGGCTATGACATCAATATGATGAGTGCACCTCAACTGACTGCAACT 2700
DB 2641 TCTGGGCGGCTATGACATCAATATGATGAGTGCACCTCAACTGACTGCAACT 2700
QY 2701 ATCTGGGCTCGGACAGTCTTGAACCGGAGAGGCTGAGCGGCTGCTGCTG 2760
DB 2701 ATCTGGGCTCGGACAGTCTTGAACCGGAGAGGCTGAGCGGCTGCTGCTG 2760
QY 2761 CTGCGCACCGCTACGCTCGGGATCGCTCACCTGCGCATCCAAACATCGAGGAGGTG 2820
DB 2761 CTGCGCACCGCTACGCTCGGGATCGCTCACCTGCGCATCCAAACATCGAGGAGGTG 2820
QY 2821 GCTCTGTGAGCATGAGAAATCCCTTTTATGCGAAAGCCATCCCATCGAGCCATC 2880
DB 2821 GCTCTGTGAGCATGAGAAATCCCTTTTATGCGAAAGCCATCCCATCGAGCCATC 2880
QY 2881 AAGGGGAGGAGGACCTCTTTTCTGCGCATTTTCAAGAGAAATGTGATGAGTGTGCGG 2940

Dd	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAAGAAATGTGATGAGCTCGCCGG	2940	4021	TGGAATTTTCATCAGCGGGATACAATATTATAGAGGCTTGTCCACTCTGCTGGCAACCC	4080	
Qy	2941	AAGCTGTCCGGCTCGGACTCAAGTGTAGACATATTACGGGGCCCTTGATGTATCCGTC	3000	Dd	4021	TGGAATTTTCATCAGCGGGATACAATATTATAGAGGCTTGTCCACTCTGCTGGCAACCC	4080
Dd	2941	AAGCTGTCCGGCTCGGACTCAATGCTAGCATATTACGGGGCCCTTGATGTATCCGTC	3000	Qy	4081	GGATAGCATCATGATGGCATTCAGAGCTCTATCACCAGCCGCTCACCAACCAACAT	4140
Qy	3001	ATACCAACTAGCGGAGACGTCAATGCTAGCAACGGAAGCTCTAATGACGGGCTTTACC	3060	Dd	4081	GGATAGCATCATGATGGCATTCAGAGCTCTATCACCAGCCGCTCACCAACCAACAT	4140
Dd	3001	ATACCAACTAGCGGAGACGTCAATGCTAGCAACGGAAGCTCTAATGACGGGCTTTACC	3060	Qy	4141	ACCTCTCTTTAAACATCTGGGGGATGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
Qy	3061	GGCGATTTCCAGTCACTGATCGACTGCAATACATGTGTACCCAGACAGTCACTTCAGC	3120	Dd	4141	ACCTCTCTTTAAACATCTGGGGGATGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
Dd	3061	GGCGATTTCCAGTCACTGATCGACTGCAATACATGTGTACCCAGACAGTCACTTCAGC	3120	Qy	4201	GCTTCTGCTTTCTAGCGCCGCGCATCGCTGGAGCGGCTTGTGGCAGCATAGGCTTTGGG	4260
Qy	3121	CTGGACCCGACCTTCAACATTTAGAGACGACCGTGGCAAAAGCGGGTGTACGCTCG	3180	Dd	4201	GCTTCTGCTTTCTAGCGCCGCGCATCGCTGGAGCGGCTTGTGGCAGCATAGGCTTTGGG	4260
Dd	3121	CTGGACCCGACCTTCAACATTTAGAGACGACCGTGGCAAAAGCGGGTGTACGCTCG	3180	Qy	4261	AAGGTGCTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGGGCC	4320
Qy	3181	CAGCGGGAGGACGACTGGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGA	3240	Dd	4261	AAGGTGCTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGGGCC	4320
Dd	3181	CAGCGGGAGGACGACTGGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGA	3240	Qy	4321	TTTAAAGTCAATAGCGCGAGATGCCCTCCACCGAGACCTGTGTTAACTACTCTCCCTGCT	4380
Qy	3241	GAACGGCCCTCGGCGATTTGATTTCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGT	3300	Dd	4321	TTTAAAGTCAATAGCGCGAGATGCCCTCCACCGAGACCTGTGTTAACTACTCTCCCTGCT	4380
Dd	3241	GAACGGCCCTCGGCGATTTGATTTCTCGGTTCTGTGCGAGTGTCTATGACGCGGGCTGT	3300	Qy	4381	ATCCTCTCCCTCGCGCCCTAGTCTCGGGGCTGTGTGCGCAGCGATCTGCTGCGCAC	4440
Qy	3301	GCTTGGTACGAGTCAACGCGCGGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360	Dd	4381	ATCCTCTCCCTCGCGCCCTAGTCTCGGGGCTGTGTGCGCAGCGATCTGCTGCGCAC	4440
Dd	3301	GCTTGGTACGAGTCAACGCGCGGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360	Qy	4441	GTGGCCCGAGGGAGGGGGCTGTGAGTGAACCGGGCTGTAGGCTTCCGTTCCGCG	4500
Qy	3361	CCAGGTTGCGGCTGCGCAGGACCATCTGAGTTCTGGGAGAGCGTCTTTACAGGCTC	3420	Dd	4441	GTGGCCCGAGGGAGGGGGCTGTGAGTGAACCGGGCTGTAGGCTTCCGTTCCGCG	4500
Dd	3361	CCAGGTTGCGGCTGCGCAGGACCATCTGAGTTCTGGGAGAGCGTCTTTACAGGCTC	3420	Qy	4501	GGTAAACACGCTCCCGACGCACTATGTGCTCAGAGCGACGCTGCAGCACGTTGCTCACT	4560
Qy	3421	ACCCACATAGACGCGCCATTTCTTCTCCAGACTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Dd	4501	GGTAAACACGCTCCCGACGCACTATGTGCTCAGAGCGACGCTGCAGCACGTTGCTCACT	4560
Dd	3421	ACCCACATAGACGCGCCATTTCTTCTCCAGACTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Qy	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGGCTTCCACAGTGTATCAAC	4620
Qy	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC	3540	Dd	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGGCTTCCACAGTGTATCAAC	4620
Dd	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC	3540	Qy	4621	GAGACTGTCTCAGCCCATGCTCCGGCTCAGGCTGTGGGCTAGAGATGTTTGGGATGATGTC	4680
Qy	3541	CAATGTGGAGTGTCTCATAGGCTAAAGCTACGCTGACAGGCGCAACGCCCTCTGCTG	3600	Dd	4621	GAGACTGTCTCAGCCCATGCTCCGGCTCAGGCTGTGGGCTAGAGATGTTTGGGATGATGTC	4680
Dd	3541	CAATGTGGAGTGTCTCATAGGCTAAAGCTACGCTGACAGGCGCAACGCCCTCTGCTG	3600	Qy	4681	ACGCTGTTGACTGATTTCAAGACCTGTGCTCAGTCCAGCTCCTGCCCGATTTGCCGGGA	4740
Qy	3601	TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Dd	4681	ACGCTGTTGACTGATTTCAAGACCTGTGCTCAGTCCAGCTCCTGCCCGATTTGCCGGGA	4740
Dd	3601	TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Qy	4741	GTCCCTTCTTCTCATGTCAAAGGGGTAAGGGAGTCTGGCGGGGAGCGGCTATG	4800
Qy	3661	ATGGCATGATGTCCGCTGACCTGAGTGTCTGACAGCACTGGGCTGTGATAGGCGGA	3720	Dd	4741	GTCCCTTCTTCTCATGTCAAAGGGGTAAGGGAGTCTGGCGGGGAGCGGCTATG	4800
Dd	3661	ATGGCATGATGTCCGCTGACCTGAGTGTCTGACAGCACTGGGCTGTGATAGGCGGA	3720	Qy	4801	CAAAACCACTGCCATGTGGAGCAGATCACCGGACATGTGAAACCGTTCATGAGG	4860
Qy	3721	GTCTAGCAGCTCTGCGCGGATTTGCTGACACAGCAGCGGTGCTATTTGGGCGAGG	3780	Dd	4801	CAAAACCACTGCCATGTGGAGCAGATCACCGGACATGTGAAACCGTTCATGAGG	4860
Dd	3721	GTCTAGCAGCTCTGCGCGGATTTGCTGACACAGCAGCGGTGCTATTTGGGCGAGG	3780	Qy	4861	ATCTGGGGCCCTTAGGACCTGTAGTAAACACGTTGGGCAATTCCTCCATTAACCGGTAC	4920
Qy	3781	ATCATCTTGTCCGGAAAGCGGCGCATTTCCCGACAGGGAAGTCTTTACCGGGAGTTC	3840	Dd	4861	ATCTGGGGCCCTTAGGACCTGTAGTAAACACGTTGGGCAATTCCTCCATTAACCGGTAC	4920
Dd	3781	ATCATCTTGTCCGGAAAGCGGCGCATTTCCCGACAGGGAAGTCTTTACCGGGAGTTC	3840	Qy	4921	ACCACGGGCGCTGTGACGCGCTTCCCGCGCCCAATTTATTCTAGGGCGCTGTGGCGGTG	4980
Qy	3841	GATGAGATGGAGTGGCGCTTCAACCTCCCTTACATCGAACAGGAGTACGCTCGCC	3900	Dd	4921	ACCACGGGCGCTGTGACGCGCTTCCCGCGCCCAATTTATTCTAGGGCGCTGTGGCGGTG	4980
Dd	3841	GATGAGATGGAGTGGCGCTTCAACCTCCCTTACATCGAACAGGAGTACGCTCGCC	3900	Qy	4981	GCTGTGAGGAGTACGCGGTTACGCGGTTGGGGATTTTCCACTACGTGACGGGCTATG	5040
Qy	3901	GAACAATTCAAACAGAAAGCAATCGGCTGCTGCAAAACAGCCCAACGAAGCGGAGCT	3960	Dd	4981	GCTGTGAGGAGTACGCGGTTACGCGGTTGGGGATTTTCCACTACGTGACGGGCTATG	5040
Dd	3901	GAACAATTCAAACAGAAAGCAATCGGCTGCTGCAAAACAGCCCAACGAAGCGGAGCT	3960	Qy	5041	ACCACTGACAAGTAAAGTCCCGGTGTAGGTTCCCGGCGCCCGAATTTCTTACAGAGT	5100
Qy	3961	GCTGTCTCCGTTGGTGAATTCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAAGCATG	4020	Dd	5041	ACCACTGACAAGTAAAGTCCCGGTGTAGGTTCCCGGCGCCCGAATTTCTTACAGAGT	5100
Dd	3961	GCTGTCTCCGTTGGTGAATTCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAAGCATG	4020				

QY 5101 GATGGGTGCGGTTGCA CAGGTACGCTCCAGCGTGCAAAACCCCTCTCTACGGGAGGAGTTC 5160
Db 5101 GATGGGGTTCGGGTGTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTCTACGGGAGGAGTTC 5160
QY 5161 ACATTCCTGCTGCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATGCCAGCCGGA 5220
Db 5161 ACATTCCTGCTGCGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATGCCAGCCGGA 5220
QY 5221 CGGACGTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCACATACGGCGGAGACG 5280
Db 5221 CGGACGTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCACATACGGCGGAGACG 5280
QY 5281 GCTAAGCCTAGCTGCGGCTGCGGAGGATCTCCCGCTCTGTCGCGAGTCACTACGCTAGCCAG 5340
Db 5281 GCTAAGCCTAGCTGCGGCTGCGGAGGATCTCCCGCTCTGTCGCGAGTCACTACGCTAGCCAG 5340
QY 5341 CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGAC 5400
Db 5341 CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGAC 5400
QY 5401 CTCAATCGAGGCAACCTCTGTCGCGGAGGATGCGGCGGGAACATCACCGCGTGGAG 5460
Db 5401 CTCAATCGAGGCAACCTCTGTCGCGGAGGATGCGGCGGGAACATCACCGCGTGGAG 5460
QY 5461 TCAGAAATAGGTAGTAATTTGGACTCTTTGAGCGCGCTCCAGCGGAGGATGAG 5520
Db 5461 TCAGAAATAGGTAGTAATTTGGACTCTTTGAGCGCGCTCCAGCGGAGGATGAG 5520
QY 5521 AGGGAAGTATCCGTTCCGCGGAGATCTGCGGAGGTCAGGAAATCCCTCGAGCGATG 5580
Db 5521 AGGGAAGTATCCGTTCCGCGGAGATCTGCGGAGGTCAGGAAATCCCTCGAGCGATG 5580
QY 5581 CCCATATGGGCAACCCCGGATTAACAACCTCCACTGTTAGAGTCTGGAAGAACCCCGAC 5640
Db 5581 CCCATATGGGCAACCCCGGATTAACAACCTCCACTGTTAGAGTCTGGAAGAACCCCGAC 5640
QY 5641 TACGTCCTTCAGTGTACAGGCTGTCATGTCGCGCTCCAGAGGCGCTCCCATACCA 5700
Db 5641 TACGTCCTTCAGTGTACAGGCTGTCATGTCGCGCTCCAGAGGCGCTCCCATACCA 5700
QY 5701 CCTCCAGGAGAGAGAGGTTGCTGTCAGAACTACCGGTCCGACAGCGGACACGSCA 5760
Db 5701 CCTCCAGGAGAGAGAGGTTGCTGTCAGAACTACCGGTCCGACAGCGGACACGSCA 5760
QY 5761 GAGTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCGTCGACAGCGGACACGSCA 5820
Db 5761 GAGTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCGTCGACAGCGGACACGSCA 5820
QY 5821 ACGGCTCTCTGACAGCCCTCCGACGAGCGGCGGATCCGACGCTTGAAGTCTGAC 5880
Db 5821 ACGGCTCTCTGACAGCCCTCCGACGAGCGGCGGATCCGACGCTTGAAGTCTGAC 5880
QY 5881 TCCTTCCATGCCCCCTTGAAGGGAGCGCGGGGATCCCGATCTCAGGAGCGGTCTTGG 5940
Db 5881 TCCTTCCATGCCCCCTTGAAGGGAGCGCGGGGATCCCGATCTCAGGAGCGGTCTTGG 5940
QY 5941 TCTACCGTAAGCGAGGAGGCTAGTGAGGACGTCTGCTGCTGCTGCTGCTACATGG 6000
Db 5941 TCTACCGTAAGCGAGGAGGCTAGTGAGGACGTCTGCTGCTGCTGCTGCTACATGG 6000
QY 6001 ACAGGCGCTCTGATCAGCCATGCGGTCGCGGAGAAACCAAGCTGCCCATCAATGCACTG 6060
Db 6001 ACAGGCGCTCTGATCAGCCATGCGGTCGCGGAGAAACCAAGCTGCCCATCAATGCACTG 6060
QY 6061 AGCAACTCTTTGCTCCGTCACCACTGCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 6120
Db 6061 AGCAACTCTTTGCTCCGTCACCACTGCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 6120
QY 6121 CTGCGGAGAGAGGTCACCTTTGACAGACTGAGGTCCTGAGCGACCACTACCGGGAC 6180
Db 6121 CTGCGGAGAGAGGTCACCTTTGACAGACTGAGGTCCTGAGCGACCACTACCGGGAC 6180
QY 6181 GTGCTCAGGAGATGAGGCGAGGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG 6240

Db 6181 GTGCTCAGGAGATGAGGCGAGGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG 6240
QY 6241 GAAGCCTGTAGCTCAGCCCCCACCATTGCGGCAGATCTAAATTTGGCTATATGGGCAAG 6300
Db 6241 GAAGCCTGTAGCTCAGCCCCCACCATTGCGGCAGATCTAAATTTGGCTATATGGGCAAG 6300
QY 6301 GACGTCGCGAACCTTATCCAGCAGGCGGTTAAACCATCCGCTCCGTGTGGAAGGACTTG 6360
Db 6301 GACGTCGCGAACCTTATCCAGCAGGCGGTTAAACCATCCGCTCCGTGTGGAAGGACTTG 6360
QY 6361 CTGGAAGACACTGAGACACCAATTGACACCAACCATCATGCGAAAAATGAGGTTTTCTGC 6420
Db 6361 CTGGAAGACACTGAGACACCAATTGACACCAACCATCATGCGAAAAATGAGGTTTTCTGC 6420
QY 6421 GTCCAAACAGAGAGGCGGCGAAGCCAGTCGCTTATCGTATTCAGATTTGGG 6480
Db 6421 GTCCAAACAGAGAGGCGGCGAAGCCAGTCGCTTATCGTATTCAGATTTGGG 6480
QY 6481 GTTCGTGTGCGGAGAAATGGCCCTTTACGATGTGTCCTCAACCTCCCTCAGGCCGTG 6540
Db 6481 GTTCGTGTGCGGAGAAATGGCCCTTTACGATGTGTCCTCAACCTCCCTCAGGCCGTG 6540
QY 6541 ATGGGCTCTTCATACGGATTCCAAATACCTCTCTCGACAGCGGTCGAGTCTCTGTGAA 6600
Db 6541 ATGGGCTCTTCATACGGATTCCAAATACCTCTCTCGACAGCGGTCGAGTCTCTGTGAA 6600
QY 6601 GCCTGGAAGCGAAGAAATGCGCTATGGCTTCGATATGACACCGCTGTTTGACTCA 6660
Db 6601 GCCTGGAAGCGAAGAAATGCGCTATGGCTTCGATATGACACCGCTGTTTGACTCA 6660
QY 6661 ACAGTCTAGTGAATGACATCCGCTGTTGAGAGTCAATCTACCAATGTTGACTTGCC 6720
Db 6661 ACAGTCTAGTGAATGACATCCGCTGTTGAGAGTCAATCTACCAATGTTGACTTGCC 6720
QY 6721 CCCAAGCCAGACAGGCGCATTAAGGTCGCTACAGAGCGGCTTACATCGGGGCGCCCTG 6780
Db 6721 CCCAAGCCAGACAGGCGCATTAAGGTCGCTACAGAGCGGCTTACATCGGGGCGCCCTG 6780
QY 6781 ACTAATTTCTAAGGCGAGAACTGCGGCTATGCGCGTTCGCGCGAGCGGTGTACTGACG 6840
Db 6781 ACTAATTTCTAAGGCGAGAACTGCGGCTATGCGCGTTCGCGCGAGCGGTGTACTGACG 6840
QY 6841 ACCAGCTGCGGTATACCTCTCAGATGTTACTTGAAGCGCGTTCGCGCTGTGAGCTGCG 6900
Db 6841 ACCAGCTGCGGTATACCTCTCAGATGTTACTTGAAGCGCGTTCGCGCTGTGAGCTGCG 6900
QY 6901 AAGCTCCAGGACTGCAGATGCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
Db 6901 AAGCTCCAGGACTGCAGATGCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
QY 6961 GCGGGACCCAGAGGACGAGGCGCTACGCGCTTCACGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCAGAGGACGAGGCGCTACGCGCTTCACGAGGCTATGACTAGATAC 7020
QY 7021 TCTGCCCCCTTGGGACCGCCCAACAGATACGACTTGAAGTGTATCAATATGC 7080
Db 7021 TCTGCCCCCTTGGGACCGCCCAACAGATACGACTTGAAGTGTATCAATATGC 7080
QY 7081 TCCTTCCAAATGTGTCAGTTCGCGCACGATGCTCTGGGAAAAAGGTTACTATCTCACCCGT 7140
Db 7081 TCCTTCCAAATGTGTCAGTTCGCGCACGATGCTCTGGGAAAAAGGTTACTATCTCACCCGT 7140
QY 7141 GACCCACACACCCCTTGGCGGGGTGCTGGGAGACAGCTAGACACACTCCAGTCAAT 7200
Db 7141 GACCCACACACCCCTTGGCGGGGTGCTGGGAGACAGCTAGACACACTCCAGTCAAT 7200
QY 7201 TCCTGCTAGGCAACATCATGATGTCGCCCACTTGTGGCAAGGATGATCTGATG 7260
Db 7201 TCCTGCTAGGCAACATCATGATGTCGCCCACTTGTGGCAAGGATGATCTGATG 7260
QY 7261 ACTCAATTTCTTCTCCACTCTTAGCTCAGGAACAACTTGAAGAAAGCCCTAGATCTCAG 7320

Db 7261 ACTATTTCTTCTCCATCTTCTAGCTCAGGACAACTTTGAAAAGCCCTAGATTGTCAG 7320
Qy 7321 ATCTAGGGGCGCTGTATCTCAATTTAGCCACTTGACCTTACCTCAGATCAATCAACGACTC 7380
Db 7321 ATCTAGGGGCGCTGTATCTCAATTTAGCCACTTGACCTTACCTCAGATCAATCAACGACTC 7380
Qy 7381 CATGGCTTAGCGCAATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Db 7381 CATGGCTTAGCGCAATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Qy 7441 TCATGGCTCAGGAAACTTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGGGCCAGAACT 7500
Db 7441 TCATGGCTCAGGAAACTTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGGGCCAGAACT 7500
Qy 7501 GTCGGCTTAGGCTACTGTCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCGGCTTAGGCTACTGTCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Qy 7561 AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAACTCCGCTGCGTCCCAAGTTGGAT 7620
Db 7561 AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAACTCCGCTGCGTCCCAAGTTGGAT 7620
Qy 7621 TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
Qy 7681 GCGCGACCCGCTGGTTCATGTGCTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCGCGACCCGCTGGTTCATGTGCTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT 7740
Qy 7741 CTACTCCCAACCGATCAACCGGGAGCTAAACCTCCAGGCCAATAGGCCATCTCTGTTT 7800
Db 7741 CTACTCCCAACCGATCAACCGGGAGCTAAACCTCCAGGCCAATAGGCCATCTCTGTTT 7800
Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Qy 7861 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Qy 7921 TAGCTGTGAAGTCCGCTGAGCCCTTGACTGCGAGAGTGTCTGATCTGGCCCTCTCTGC 7980
Db 7921 TAGCTGTGAAGTCCGCTGAGCCCTTGACTGCGAGAGTGTCTGATCTGGCCCTCTCTGC 7980
Qy 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 14

ADP86271
ID ADP86271 standard; DNA; 11313 BP.

XX AC

XX ADP86271;

XX DT

XX 23-SEP-2004 (first entry)

XX DE

XX Hepatitis C virus Con-1 replicon I377/NS3-3' derived plasmid DNA, p2S10.

XX KW

XX Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;

XX KW

XX ds.

XX OS

XX Hepatitis C virus.

XX PN

XX WO200405216-A2.

XX XX

XX 01-JUL-2004.

XX PD

XX 12-DEC-2003; 2003WO-US039722.

XX XX

XX 13-DEC-2002; 2002US-0433303P.

XX (FOX-) FOX CHASE CANCER CENT.

XX PI

XX Zhu Q, Guo J, Seeger C;

XX DR

XX WPI; 2004-488079/46.

XX New cell-line that replicates hepatitis C virus (HCV), where the cell

line is selected from a non-human cell line and a human non-hepatic cell

line, useful for identifying anti-HCV agents for treating HCV infections.

XX Example III; SEQ ID NO 8; 130pp; English.

XX The present invention provides hepatitis C virus (HCV) replication cells

and cell lines derived from human non-hepatic cells or non-human cells.

XX The invention is useful for identifying anti-HCV agents for treating HCV

infections. The present sequence is hepatitis C virus Con-1 replicon

CC I377/NS3-3' derived plasmid DNA.

XX Sequence 11313 BP; 2346 A; 3334 C; 3153 G; 2480 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 7988.8; DB 12; Length 11313;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGCCCCGATTTGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

Db 1 GCCAGCCCCGATTTGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

Qy 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120

Db 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120

Qy 121 CCCCTCCGCGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAAATGGCAG 180

Db 121 CCCCTCCGCGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAAATGGCAG 180

Qy 181 GAGCAGCGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTGCCTCC 240

Db 181 GAGCAGCGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTGCCTCC 240

Qy 241 GCGAGATCTAGCCGAGTAGTGTGGTCCGAAAGGCTTGTGGTACTGCTCTGATAGG 300

Db 241 GCGAGATCTAGCCGAGTAGTGTGGTCCGAAAGGCTTGTGGTACTGCTCTGATAGG 300

Qy 301 GTGCTTCGAGTGCCTCCGCGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCTTAAAC 360

Db 301 GTGCTTCGAGTGCCTCCGCGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCTTAAAC 360

Qy 361 CTCAAGAGAAACCAAAGGGCGCCCATGATTAACCAAGATGGAATGACCGAGGTTCTC 420

Db 361 CTCAAGAGAAACCAAAGGGCGCCCATGATTAACCAAGATGGAATGACCGAGGTTCTC 420

Qy 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAGACAAATCGCTGCT 480

Db 421 CGGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAGACAAATCGCTGCT 480

Qy 481 CTGATGCGCGCTGTTCGGCTGTGAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540

Db 481 CTGATGCGCGCTGTTCGGCTGTGAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540

Qy 541 ACCTGTCCGCTGCTTGAATGAACTGCAAGACGAGGCGCGGCTATCGTGGTGGCCA 600

Db 541 ACCTGTCCGCTGCTTGAATGAACTGCAAGACGAGGCGCGGCTATCGTGGTGGCCA 600

Qy 601 CGAGGGGCTTCCCTTGGCGAGCTGTGCTCGAGTGTCTGAGAGGAGGAGCTGCTGCT 660

Db 601 CGAGGGGCTTCCCTTGGCGAGCTGTGCTCGAGTGTCTGAGAGGAGGAGCTGCTGCT 660

Qy 661 TGCTATTGGCGAAGTGCCTGGCGAGGATCTCTGCTCATCTCACCTTCTCTGCGGAGA 720

Db 661 TGCTATTGGCGAAGTGCCTGGCGAGGATCTCTGCTCATCTCACCTTCTCTGCGGAGA 720

QY 721 AAGTATCCATATGCGTGTGATGCAATGCGCGGCTGCATACGCTTGATCGCGTACTCGC 780
Db 721 AAGTATCCATATGCGTGTGATGCAATGCGCGGCTGCATACGCTTGATCGCGTACTCGC 780
QY 781 CATTCGACCAACAGCGAAACATCCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACAGCGAAACATCCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCCG 900
Db 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCCG 900
QY 901 CCAGGCTCAAGCGCGCATGCCCCGACGCGAGGATCTCGTGTGACCCATGCGATGCGT 960
Db 901 CCAGGCTCAAGCGCGCATGCCCCGACGCGAGGATCTCGTGTGACCCATGCGATGCGT 960
QY 961 GCTTCCCGAATATCATGTGGAAATGCGCGTCTTCTGGATTCACTGATGCTGCGCGG 1020
Db 961 GCTTCCCGAATATCATGTGGAAATGCGCGTCTTCTGGATTCACTGATGCTGCGCGG 1020
QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATATTTGCTGAAGAGC 1080
Db 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATATTTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGGCTGACCGCTTCTCGTGTCTTACGTTATCGCGCTCCCGATTCCG 1140
Db 1081 TTGGCGGGAATGGCTGACCGCTTCTCGTGTCTTACGTTATCGCGCTCCCGATTCCG 1140
QY 1141 AGCGCATCGCCTTCTATCGCCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACACACG 1200
Db 1141 AGCGCATCGCCTTCTATCGCCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACACACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTTAAAGTTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTTAAAGTTACTGCG 1260
QY 1261 CGAAGCGCTTGAATTAAGCGCGGTGCGTTGTCTATATGTTATTTTCCACCATATTG 1320
Db 1261 CGAAGCGCTTGAATTAAGCGCGGTGCGTTGTCTATATGTTATTTTCCACCATATTG 1320
QY 1321 CCGTCTTTTGGCAATGTAGAGCGCCGGAACCTCGGCCCTGTCTTCTTGAAGAGATTCT 1380
Db 1321 CCGTCTTTTGGCAATGTAGAGCGCCGGAACCTCGGCCCTGTCTTCTTGAAGAGATTCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGTCTGTAAGGAAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGTCTGTAAGGAAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGTCTGTAGCGACCTTTGACGACGCG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGTCTGTAGCGACCTTTGACGACGCG 1500
QY 1501 AACCCCCCACTGCGGACAGTGTCTCTGCGGCCAAAGCCAGCTGTATAGATACACCT 1560
Db 1501 AACCCCCCACTGCGGACAGTGTCTCTGCGGCCAAAGCCAGCTGTATAGATACACCT 1560
QY 1561 GCAAGCGGCAAAACCCAGTGCCAGCTGTGAGTTGATGTTGGAAGAGTCAAA 1620
Db 1561 GCAAGCGGCAAAACCCAGTGCCAGCTGTGAGTTGATGTTGGAAGAGTCAAA 1620
QY 1621 TGCGCTCTCTCAGCGCTTCAACAGGGGCTGAGGATGCCAGAGGATACCCATTGT 1680
Db 1621 TGCGCTCTCTCAGCGCTTCAACAGGGGCTGAGGATGCCAGAGGATACCCATTGT 1680
QY 1681 ATGGGATCTGATCTGGGGCTCGGTGACATGCTTTTACATGCTGTTAGTGCAGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGGCTCGGTGACATGCTTTTACATGCTGTTAGTGCAGGTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGGAACACGCGGACGTGGTTTCTTTTGAAGAACACGATATACC 1800
Db 1741 AACGTCTAGGCCCCCGGAACACGCGGACGTGGTTTCTTTTGAAGAACACGATATACC 1800
QY 1801 ATGGCGCTATTAGGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTSCATCATCT 1860

Db 1801 ATGGCGCTATTAGGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCAATCATCT 1860
QY 1861 AGCCTCAACAGCGCGGACAGGAACACAGGTTCGAGGGGAGGTCCAAAGTGGTCTCCACCGCA 1920
Db 1861 AGCCTCAACAGCGCGGACAGGAACACAGGTTCGAGGGGAGGTCCAAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAAATCTTCTTGGCGACCTGCGTCAATGCGGTGTGTTGACACTGTCTATCATGGTGC 1980
Db 1921 ACACAAATCTTCTTGGCGACCTGCGTCAATGCGGTGTGTTGACACTGTCTATCATGGTGC 1980
QY 1981 GGCCTCAAAAGACCTTTCGCGGCCAAAGGCGCCCAATCACCCCAAAATGTACCCAAATGTGGAC 2040
Db 1981 GGCCTCAAAAGACCTTTCGCGGCCAAAGGCGCCCAATCACCCCAAAATGTACCCAAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTGCG 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTGCG 2100
QY 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGCATGCGCGATGTCAATTCGCGTGC CGCGCGG 2160
Db 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGCATGCGCGATGTCAATTCGCGTGC CGCGCGG 2160
QY 2161 GGCAGCAGCAGCGGAGCGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTTCG 2220
Db 2161 GGCAGCAGCAGCGGAGCGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTTCG 2220
QY 2221 GGCAGTCTCACTGCTCTGCGGCGCAGCTGTGGGCACTCTTTCGGGCTGCGCGTGTGC 2280
Db 2221 GGCAGTCTCACTGCTCTGCGGCGCAGCTGTGGGCACTCTTTCGGGCTGCGCGTGTGC 2280
QY 2281 ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG 2340
QY 2341 CCGTCTCCCGGCTCTTCAAGCAACTCTGCTCCCTCCGCGCGTACCGAGACATTCAGGTG 2400
Db 2341 CCGTCTCCCGGCTCTTCAAGCAACTCTGCTCCCTCCGCGCGTACCGAGACATTCAGGTG 2400
QY 2401 GCCCATCTACCGCCCTACTGTGAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA 2460
Db 2401 GCCCATCTACCGCCCTACTGTGAGCGGCAAGAGCACTAAGGTGCGCGCTGCGTATGCA 2460
QY 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGGTCCGTCGCGCGCACTTCTAGGTTCGGG 2520
Db 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGGTCCGTCGCGCGCACTTCTAGGTTCGGG 2520
QY 2521 GCGTATATGTCTAAGGCACATGTTATCGACCTTAAACATCAGAACCGGGGTAAAGACCATC 2580
Db 2521 GCGTATATGTCTAAGGCACATGTTATCGACCTTAAACATCAGAACCGGGGTAAAGACCATC 2580
QY 2581 ACCAGGGTCCCGCATACGTAATCCACTTCCACTATGGAAGTTCCTTTCGCGAGCGTGTGC 2640
Db 2581 ACCAGGGTCCCGCATACGTAATCCACTTCCACTATGGAAGTTCCTTTCGCGAGCGTGTGC 2640
QY 2641 TCTGGGGCGCCTTATGACATCAATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGCGCCTTATGACATCAATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
QY 2701 ATCCTGGGCATCGGCAAGTCTTGGACCAAGCGGAGACGCGTGGAGCGGCTGCTGCTG 2760
Db 2701 ATCCTGGGCATCGGCAAGTCTTGGACCAAGCGGAGACGCGTGGAGCGGCTGCTGCTG 2760
QY 2761 CTCGCCACCGCTACGCGTCCGGATCGGTCAACGTCACATCCAAACATTCGAGGAGGTG 2820
Db 2761 CTCGCCACCGCTACGCGTCCGGATCGGTCAACGTCACATCCAAACATTCGAGGAGGTG 2820
QY 2821 GCTCTCTCAGACCTGGAGAAATCCCTTTTATGGAAGGCAATCCCATTCGAGACCAATC 2880
Db 2821 GCTCTCTCAGACCTGGAGAAATCCCTTTTATGGAAGGCAATCCCATTCGAGACCAATC 2880
QY 2881 AAGGGGGGAGGACCTCTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGCG 2940

Db 2881 AAGGGGGGAGCACCCTCATTTTCTGCCATTCCAAAGAGAAATGTGATGAGCTCGCCGG 2940
Qy 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGTATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGTATCCGTC 3000
Qy 3001 ATACCACTAGCGGAGACGTCTATGCTGTAGCAACGGAGCTCTAATGACGGCTTTTACC 3060
Db 3001 ATACCACTAGCGGAGACGTCTATGCTGTAGCAACGGAGCTCTAATGACGGCTTTTACC 3060
Qy 3061 GCGATTTCCGACTCAGTGTACGACTGCAATACATGTGTCAACCAGACAGTTCGACTTCAG 3120
Db 3061 GCGATTTCCGACTCAGTGTACGACTGCAATACATGTGTCAACCAGACAGTTCGACTTCAG 3120
Qy 3121 CTGGACCCGACCTTCAACATTGAGACGACGACCGTGCACAGACGGGTGTACGCTCG 3180
Db 3121 CTGGACCCGACCTTCAACATTGAGACGACGACCGTGCACAGACGGGTGTACGCTCG 3180
Qy 3181 CAGCGGAGGAGGAGCTGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGAGGAGGAGCTGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Qy 3241 GAACGGCCCTCGGCACTGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Db 3241 GAACGGCCCTCGGCACTGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Qy 3301 GCTTGTAACGAGTCAAGCCGCGGAGACCTCAGTTAGTTGCGGCTTACCTAAACACA 3360
Db 3301 GCTTGTAACGAGTCAAGCCGCGGAGACCTCAGTTAGTTGCGGCTTACCTAAACACA 3360
Qy 3361 CCAGGTTGCGCTCTGSCAGGACCACTCTGAGTTCTGCGAGAGCGTCTTTACAGGCTC 3420
Db 3361 CCAGGTTGCGCTCTGSCAGGACCACTCTGAGTTCTGCGAGAGCGTCTTTACAGGCTC 3420
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Db 3421 ACCACATAGACGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
Qy 3481 CTGTTAGCATACAGGCTACGTTGTGCGCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Db 3481 CTGTTAGCATACAGGCTACGTTGTGCGCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Qy 3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTTACGCTACAGGCGCCAAAGCCCTCTG 3600
Db 3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTTACGCTACAGGCGCCAAAGCCCTCTG 3600
Qy 3601 TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC 3660
Db 3601 TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC 3660
Qy 3661 ATGGCATGCATGTCGGCTGACCTGGAGTGTCTCAGGACGCTGGGTCTGGTAGGCGGA 3720
Db 3661 ATGGCATGCATGTCGGCTGACCTGGAGTGTCTCAGGACGCTGGGTCTGGTAGGCGGA 3720
Qy 3721 GTCTAGCAGTCTTGGCGCGTATTGCTGACACAGGAGCGTGGTCAITTTGGGCGAG 3780
Db 3721 GTCTAGCAGTCTTGGCGCGTATTGCTGACACAGGAGCGTGGTCAITTTGGGCGAG 3780
Qy 3781 ATCATCTTTGTCGGAAAGCCGCGCATCATCTCCCGACAGGAGTCTTTACGGGAGTTC 3840
Db 3781 ATCATCTTTGTCGGAAAGCCGCGCATCATCTCCCGACAGGAGTCTTTACGGGAGTTC 3840
Qy 3841 GATGATGTGAGAGTGGCTCCACCTCCCTTACATCGAACAGGAAATGCACTCGCC 3900
Db 3841 GATGATGTGAGAGTGGCTCCACCTCCCTTACATCGAACAGGAAATGCACTCGCC 3900
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Db 3901 GAACAATTCAACAGAGGCAATCGGTTGCTGCAAAACAGGCCAACAGCGAGGCT 3960
Qy 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTCTGGCGAGCATATG 4020
Db 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTCTGGCGAGCATATG 4020

Qy 4021 TGGAAATTTTCATCAGCGGGATACAAATATTTAGCAGGCTGTGTCCACTCTGCTGGCAACCC 4080
Db 4021 TGGAAATTTTCATCAGCGGGATACAAATATTTAGCAGGCTGTGTCCACTCTGCTGGCAACCC 4080
Qy 4081 GCGATAGCATCTACTGATGGCAITTCAGAGCTCTATCACCAGCCGCTACCAACCAACAT 4140
Db 4081 GCGATAGCATCTACTGATGGCAITTCAGAGCTCTATCACCAGCCGCTACCAACCAACAT 4140
Qy 4141 ACCCTCCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTCTCTCTCCACGCT 4200
Db 4141 ACCCTCCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTCTCTCTCCACGCT 4200
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Db 4201 GCTTCTGCTTTTGTAGGCGCGGCATCTGCTGAGAGCGGCTGTGCGAGCATAGGCCCTTGG 4260
Qy 4261 AAGTGTCTTGTGGATATTTTGGAGGAGGGGTGCGAGCGGCTGTGCGAGCATAGGCCCTTGG 4320
Db 4261 AAGTGTCTTGTGGATATTTTGGAGGAGGGGTGCGAGCGGCTGTGCGAGCATAGGCCCTTGG 4320
Qy 4321 TTTAAGGTCATGAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTTACTCTCTGCT 4380
Db 4321 TTTAAGGTCATGAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTTACTCTCTGCT 4380
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Qy 4561 CAGATCTCTCTAGTCTTACCATCACTCAGTCTGCTGAAGAGGCTTCAACGATGATCAAC 4620
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Db 4621 GAGGACTGTCCAGCCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGGATATGC 4680
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Db 4861 ATCGTGGGCTTAGGACCTGTAGTAAACACGTTGGATGGAAATTTCCCATTAACGCGTAC 4920
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Db 4921 ACCAGGGGCTTGGACCGCCCTCCCGGCGCAATATTTCTAGGGCGCTGTGGCGGCTG 4980
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Qy 5041 ACCACTGACAAAGTAAAGTGGCGGCTGTGAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG 5100
Db 5041 ACCACTGACAAAGTAAAGTGGCGGCTGTGAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG 5100

QY 5101 GATGGGTCGGTTCACAGGTACGCTCCAGCGTCAAAACCCCTCTCTACGGAGGAGGTC 5160
DB |||||
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DB |||||
QY 5161 ACATTCCTGGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATCGAGCCCGAA 5220
DB |||||
QY 5161 ACATTCCTGGTGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATCGAGCCCGAA 5220
DB |||||
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DB |||||
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DB |||||

DB |||||
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QY 6961 GCGGGACCCAGAGGACGAGCGGCTACGGGCTTTCAGCGAGGCTATGACTAGATAC 7020
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QY 7261 ACTCAATTTCTTCCATCTCTAGCTCAGGACACTTGAAGGCTTAACTTCTATCCGTGGAG 7320
DB |||||

DB	7261	ACTCATTTCTTCTCCTCATCTTCTAGCTCAGGACAACTTGAAAGACCTAGATTGTTCAG	7320
QY	7321	ATCTACGGGGCGCTGTACTCCATTGAGCCACTTGACCTCAGATCAATCAAGACTC	7380
DB	7321	ATCTACGGGGCGCTGTACTCCATTGAGCCACTTGACCTCAGATCAATCAAGACTC	7380
QY	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTACTCTCAGAGTGAGATCAATAGGGTGGCT	7440
DB	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTACTCTCAGAGTGAGATCAATAGGGTGGCT	7440
QY	7441	TCATGGCTCAGGAACTTGGGGTACCGGCTTTCGAGTCTGGAGACATCGGGCCAGAAGT	7500
DB	7441	TCATGGCTCAGGAACTTGGGGTACCGGCTTTCGAGTCTGGAGACATCGGGCCAGAAGT	7500
QY	7501	GTCCGGCTTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGGAAGTACCTTCTC	7560
DB	7501	GTCCGGCTTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGGAAGTACCTTCTC	7560
QY	7561	AACGGGAGTAGAGCAAGCTCAAACTCACTCCAAATCCGGCTCGTCCCAAGTTGGAT	7620
DB	7561	AACGGGAGTAGAGCAAGCTCAAACTCACTCCAAATCCGGCTCGTCCCAAGTTGGAT	7620
QY	7621	TTATCCAGCTGGTTCGTCTGTCTTACAGCGGGGAGACATATACAGCCTGTCTCGT	7680
DB	7621	TTATCCAGCTGGTTCGTCTGTCTTACAGCGGGGAGACATATACAGCCTGTCTCGT	7680
QY	7681	GCCCGACCCCGCTGGTTCATGTGGTGGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
DB	7681	GCCCGACCCCGCTGGTTCATGTGGTGGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
QY	7741	CTACTCCCAACCGATGACGGGGAGCTAAACATCCAGGCCAATAGGCCATCTCTGTTT	7800
DB	7741	CTACTCCCAACCGATGACGGGGAGCTAAACATCCAGGCCAATAGGCCATCTCTGTTT	7800
QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
DB	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
DB	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	7921	TAGCTGTGAAGTCCGCTGAGCCCTTACCTGACGAGAGTCTGATCTGACCTCTCTGC	7980
DB	7921	TAGCTGTGAAGTCCGCTGAGCCCTTACCTGACGAGAGTCTGATCTGACCTCTCTGC	7980
QY	7981	AGATCAAGTACT 7992	
DB	7981	AGATCAAGTACT 7992	
RESULT 15			
ID	AAD25322	standard; cDNA; 7989 BP.	
XX	AC	AAD25322;	
XX	DT	12-MAR-2002 (first entry)	
XX	DE	Hepatitis C virus (HCV) replbBartMan/Avall cDNA.	
XX	KW	Hepatitis C virus; HCV; transfection; infection; virus neutralisation;	
XX	KW	gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;	
XX	OS	Hepatitis C virus.	
XX	FT	Key	Location/Qualifiers
XX	FT	CDS	1801..7758
XX	FT	/tag= a	
XX	FT	/product= "HCVreplbBartMan polyprotein"	
XX	FT	7766	
XX	FT	misc_feature	
XX	FT	/*tag= b	

/note= "Nucleotide creating Availi site"

WO200189364-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-US016822.

23-MAY-2000; 2000US-00576989.

(UNIW) UNIV WASHINGTON.

Rice CM, Blight KJ;

WPI: 2002-066755/09.

P-PSDB; AAE1517.

Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequences.

Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficiency replication in cell culture, establishment of alternative animal models for tissue or species tropism, development of HCV variant replication, inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated or derivative HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replbBartMan/Avall cDNA

Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7987.4; DB 6; Length 7989;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7989; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60

DB 1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60

QY 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTCTCGTCAGCTCCAGGAC 120

DB 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTCTCGTCAGCTCCAGGAC 120

QY 121 CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180

DB 121 CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180

QY 181 GACGACCGGGTCTCTTTCTTTGGATCAACCGCTCAATGCTCGAGATTTGGGGTGCCTCC 240

DB 181 GACGACCGGGTCTCTTTCTTTGGATCAACCGCTCAATGCTCGAGATTTGGGGTGCCTCC 240

QY 241 GCAGAGCTCTAGCCGAGTAGTGTGGTCCGAAAGCCCTTGTGTAAGG 300
Db 241 GCAGAGCTGTAGCCGAGTAGTGTGGTCCGAAAGCCCTTGTGTAAGG 300
QY 301 GTGCTTCGAGTGCCTCCGAGGTCTCGTAGACCGTGCAACAGACCAATCCTAAC 360
Db 301 GTGCTTCGAGTGCCTCCGAGGTCTCGTAGACCGTGCAACAGACCAATCCTAAC 360
QY 361 CTCAGAGAAACCAAGAGCGGCCATGATTGAACAAGATGGATTGCACGCAAGTTCTC 420
Db 361 CTCAGAGAAACCAAGAGCGGCCATGATTGAACAAGATGGATTGCACGCAAGTTCTC 420
QY 421 CGCGCGCTTCGCTGGAGAGGCTATTCCGCTATGACTGGGCACACAGACAATCGGCTGCT 480
Db 421 CGCGCGCTTCGCTGGAGAGGCTATTCCGCTATGACTGGGCACACAGACAATCGGCTGCT 480
QY 481 CTGATGCGCGCTGTTCCGCTGTCTAGCGCAGAGGGCGCCGGTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCCGCTGTCTAGCGCAGAGGGCGCCGGTCTTTTGTCAAGACCG 540
QY 541 ACTGTGCGGTGCCCTGAATGAATCTGAGGACGAGGACGCGCGCTATCGTGGCTGGCCA 600
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QY 601 CGACGGGCGTTCCTTCGCGAGCTGTCTCGAAGCTGTCTGTAAGCGGGAAGGACTGGC 660
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QY 721 AAGTATCCATATGCTGTGATCAATGCGCGGCTGCTGATACGCTGTGATCCGCTACTCGCC 780
Db 721 AAGTATCCATATGCTGTGATCAATGCGCGGCTGCTGATACGCTGTGATCCGCTACTCGCC 780
QY 781 CATTTCGACCAACGAGGAAATCCGATCGACGAGACGTAAGTGGAGGCGGTC 840
Db 781 CATTTCGACCAACGAGGAAATCCGATCGACGAGACGTAAGTGGAGGCGGTC 840
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Db 841 TTGTGATCAGGATGATCTGACGAGGATCATCAGGGCTCGCGGCTCGCGGCTCGGAACTGTCG 900
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QY 1081 TTGCGCGGAATGGCTGACCGCTTCCTGCTTTACGATATCGCGCTCCCGATTGCG 1140
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Db 1141 AGCGCATCGCTTCTATCGCTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACGTTACTGGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACGTTACTGGC 1260
QY 1261 CGAAGCGCTTGGAAATAGGCGGCTGTGCTATATGTTATTTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGGAAATAGGCGGCTGTGCTATATGTTATTTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTAGGGGCCGAAACCTGGCCCTGTCTTTTACGAGCATTTCT 1380

Db 1321 CCGTCTTTTGGCAATGTAGGGGCCGAAACCTGGCCCTGTCTTTTACGAGCATTTCT 1380
QY 1381 AGGGGTCTTTCCCTCTCTCGCAAGGAATGCAAGGTCTGTGTAATGTCGTCAAGGAGCA 1440
Db 1381 AGGGGTCTTTCCCTCTCTCGCAAGGAATGCAAGGTCTGTGTAATGTCGTCAAGGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAGTGTGTAGCGACCCCTTTTCAGGACGCG 1500
Db 1441 GTTCTCTGTGAAGCTTCTTGAAGACAAACAGTGTGTAGCGACCCCTTTTCAGGACGCG 1500
QY 1501 AACCCCCCACTCGCGACAGGTCTCTCGGCCAAAGCAACAGTGTGTGAAGATACACCT 1560
Db 1501 AACCCCCCACTCGCGACAGGTCTCTCGGCCAAAGCAACAGTGTGTGAAGATACACCT 1560
QY 1561 GCAAGCGCGCAACACCCAGTGCACAGTGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
Db 1561 GCAAGCGCGCAACACCCAGTGCACAGTGTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
QY 1681 ATGGGATCTGATCTGGGCTCGGTCCACATGCTTTACATGTTTGTAGCGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCGGTCCACATGCTTTACATGTTTGTAGCGGTTAAA 1740
QY 1741 AACGCTAGGCCCCCGAACACACGCGGACGTGTTTCTTTTGAAGAACACCATATACC 1800
Db 1741 AACGCTAGGCCCCCGAACACACGCGGACGTGTTTCTTTTGAAGAACACCATATACC 1800
QY 1801 ATGGCGCTTTTACGGCTATCTCCAAACAGCGGAGGCTTACTTGGCTGCATCATCT 1860
Db 1801 ATGGCGCTTTTACGGCTATCTCCAAACAGCGGAGGCTTACTTGGCTGCATCATCT 1860
QY 1861 AGCCTCACAGCGCGGACAGGAAACAGGTCCAGGGGAGGTCAGAGTGTCTCCACCGCA 1920
Db 1861 AGCCTCACAGCGCGGACAGGAAACAGGTCCAGGGGAGGTCAGAGTGTCTCCACCGCA 1920
QY 1921 ACACAACTTTCTGCGGACCTGCGTCAATGCGGTGTGTGGAGTGTCTATCATGGTGC 1980
Db 1921 ACACAACTTTCTGCGGACCTGCGTCAATGCGGTGTGTGGAGTGTCTATCATGGTGC 1980
QY 1981 GGCTCAAGACCTTTGCGGCGCCAAAGGCGCCAATCACCCAAATGTACCAATGTGGAC 2040
Db 1981 GGCTCAAGACCTTTGCGGCGCCAAAGGCGCCAATCACCCAAATGTACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTCCGCTGSCAAGCGCCCCCGGGCGGCTTCTTGACACCATGCACTGC 2100
Db 2041 CAGGACCTCGTCCGCTGSCAAGCGCCCCCGGGCGGCTTCTTGACACCATGCACTGC 2100
QY 2101 GGCAGCTCGGACCTTTACTTTGTCACGAGGATGCCGATGTCAATTCGGTCCGCGCGG 2160
Db 2101 GGCAGCTCGGACCTTTACTTTGTCACGAGGATGCCGATGTCAATTCGGTCCGCGCGG 2160
QY 2161 GGCAGACGAGGCGGAGCTACTCTCCCGAGGCGGCTTCTTCTTGAAGGCTCTTCG 2220
Db 2161 GGCAGACGAGGCGGAGCTACTCTCCCGAGGCGGCTTCTTCTTGAAGGCTCTTCG 2220
QY 2221 GCGGCTCACTGTCTCTCCCTCGGGCAGCTGTGGGCACTTTCCGGCTCCGCTGTC 2280
Db 2221 GCGGCTCACTGTCTCTCCCTCGGGCAGCTGTGGGCACTTTCCGGCTCCGCTGTC 2280
QY 2281 ACCGAGGGTTCGAGGCGGTGGAATTTGTATCCCGTCCAGTCTATGGAACACCATATG 2340
Db 2281 ACCGAGGGTTCGAGGCGGTGGAATTTGTATCCCGTCCAGTCTATGGAACACCATATG 2340
QY 2341 CGGTCCCGCTTTCAGGACAACTCGTCCCTCCGCGGCTACCGGACATTTCCAGGTG 2400
Db 2341 CGGTCCCGCTTTCAGGACAACTCGTCCCTCCGCGGCTACCGGACATTTCCAGGTG 2400
QY 2401 GCGCATCTACGCGCTTACTGTAGCGGACGACCTAAGGTGCGGCTGCGTATGCA 2460

Db	2401	GCCCATCTACAGCCGCCCTACTGCTAGCGCAAGAGCACTAAGGTGCCGCTGCGTATGCA	2460
Qy	2461	GCCCAAGGGTATAAGGTGCTTGTCTGTAACCCGTCGTCGCCGCCACCCTAGGTTTCGGG	2520
Db	2461	GCCCAAGGGTATAAGGTGCTTGTCTGTAACCCGTCGTCGCCGCCACCCTAGGTTTCGGG	2520
Qy	2521	GGGTATATGTCTAAGGCACATGCTATCGACCTTAACATCAGAACCCGGGTAAGGACCATC	2580
Db	2521	GGGTATATGTCTAAGGCACATGCTATCGACCTTAACATCAGAACCCGGGTAAGGACCATC	2580
Qy	2581	ACCACGGGTGCCCCCATCTACGTAATCCACCTATGCGCAAGTTTCTTGCCGACGGTGTGTC	2640
Db	2581	ACCACGGGTGCCCCCATCTACGTAATCCACCTATGCGCAAGTTTCTTGCCGACGGTGTGTC	2640
Qy	2641	TCTGGGGGGCCCTATGACATCATATATATGATGAGTGCCACTCAACTGACTCGACCACT	2700
Db	2641	TCTGGGGGGCCCTATGACATCATATATATGATGAGTGCCACTCAACTGACTCGACCACT	2700
Qy	2701	ATCTTGGGCATCGGCACAGCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG	2760
Db	2701	ATCTTGGGCATCGGCACAGCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG	2760
Qy	2761	CTGCCACCGCTACGCTCCGGGATCGGTCAACGTCGCACATCCAAACATCGAGGAGGTG	2820
Db	2761	CTGCCACCGCTACGCTCCGGGATCGGTCAACGTCGCACATCCAAACATCGAGGAGGTG	2820
Qy	2821	GCTCTGTCCAGCACTGAGGAAATCCCTTTTATGCGCAAGGCAATCCCGATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGAGGAAATCCCTTTTATGCGCAAGGCAATCCCGATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGACCTTCTTCTGCCATTCCTCAAGAGGAATGATGAGCTCGCGCG	2940
Db	2881	AAGGGGGGAGGACCTTCTTCTGCCATTCCTCAAGAGGAATGATGAGCTCGCGCG	2940
Qy	2941	AAGTGTCCGGCTCGGACTCAATGCTGATGATATTAACGGGGCTTGTATCGCTC	3000
Db	2941	AAGTGTCCGGCTCGGACTCAATGCTGATGATATTAACGGGGCTTGTATCGCTC	3000
Qy	3001	ATACCAACTAGCGAGAGCTCATTTGCTGTAAGAACGAGCGCTTAATGACGGGCTTTACC	3060
Db	3001	ATACCAACTAGCGAGAGCTCATTTGCTGTAAGAACGAGCGCTTAATGACGGGCTTTACC	3060
Qy	3061	GGCGATTCGACTGACTGCAATATGCTGATGATATTAACGGGGCTTGTATCGCTC	3120
Db	3061	GGCGATTCGACTGACTGCAATATGCTGATGATATTAACGGGGCTTGTATCGCTC	3120
Qy	3121	CTGGACCCGACCTTCAACATTTAGAGACGACGACCGTGCCAAAGACGCGGTGTCAGCTCG	3180
Db	3121	CTGGACCCGACCTTCAACATTTAGAGACGACGACCGTGCCAAAGACGCGGTGTCAGCTCG	3180
Qy	3181	CAGCGCGAGGACGAGCTGTTAGGGGAGGATGGGATTTTACAGGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGCGAGGACGAGCTGTTAGGGGAGGATGGGATTTTACAGGTTTGTGACTCCAGGA	3240
Qy	3241	GAAACGGCTCGGGCATGTTCCATTCCTGCTGCTGAGTGTATGACGCGGCTGT	3300
Db	3241	GAAACGGCTCGGGCATGTTCCATTCCTGCTGCTGAGTGTATGACGCGGCTGT	3300
Qy	3301	GCTTGTGTACGAGCTCACGCGCCGCGAGACCTCAGTTAGGTGTGGGCTTACCTAAACACA	3360
Db	3301	GCTTGTGTACGAGCTCACGCGCCGCGAGACCTCAGTTAGGTGTGGGCTTACCTAAACACA	3360
Qy	3361	CCAGGTTGCCCTGTGCGAGACCATCTGGAGTTCTGGAGAGCGCTTTACAGGCTC	3420
Db	3361	CCAGGTTGCCCTGTGCGAGACCATCTGGAGTTCTGGAGAGCGCTTTACAGGCTC	3420
Qy	3421	ACCCACATAGACGCCCATTTCTTGTCCGACTAAGCAGGACGAGACCACTTCCCTTAC	3480
Db	3421	ACCCACATAGACGCCCATTTCTTGTCCGACTAAGCAGGACGAGACCACTTCCCTTAC	3480
Qy	3481	CTGGTAGCATACCAAGGCTACGGTGTGCGCAGGGCTCAGGCTCAGCTCGTGGGAC	3540
Db	3481	CTGGTAGCATACCAAGGCTACGGTGTGCGCAGGGCTCAGGCTCAGCTCGTGGGAC	3540
Qy	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTCACGGGCCAACGCCCTGCTG	3600
Db	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTCACGGGCCAACGCCCTGCTG	3600
Qy	3601	TATAGCTGGAGCGCTTCAAAACGAGGTTACTTACACACACCCATAACCAATACATC	3660
Db	3601	TATAGCTGGAGCGCTTCAAAACGAGGTTACTTACACACACCCATAACCAATACATC	3660
Qy	3661	ATGGCATCATGTCCGCTGACCTGGAGTCTGTCAGAGCACCTGGTGTGTTAGGCGGA	3720
Db	3661	ATGGCATCATGTCCGCTGACCTGGAGTCTGTCAGAGCACCTGGTGTGTTAGGCGGA	3720
Qy	3721	GTCTTAGCAGCTCTGCGCGGTATTGCTGCAACAGGAGCGCTGCTCATTTGGGCGAG	3780
Db	3721	GTCTTAGCAGCTCTGCGCGGTATTGCTGCAACAGGAGCGCTGCTCATTTGGGCGAG	3780
Qy	3781	ATCATCTTGTCCGAAAGCGGCAATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Db	3781	ATCATCTTGTCCGAAAGCGGCAATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTC	3840
Qy	3841	GATGAGATGAAAGTGGCGCTCACACCTCCCTTTACATCAACAGGGAATGCACTCGCC	3900
Db	3841	GATGAGATGAAAGTGGCGCTCACACCTCCCTTTACATCAACAGGGAATGCACTCGCC	3900
Qy	3901	GAAACAATTCAAACAGAAAGGCAATCGGGTTGTCGAAACAGCCACCAAGCGAGGCT	3960
Db	3901	GAAACAATTCAAACAGAAAGGCAATCGGGTTGTCGAAACAGCCACCAAGCGAGGCT	3960
Qy	3961	GCTGCTCCGTGTGGAAATCCAGTGGCGGACCTCGAAGGCTTCTGGGGGAAACATATG	4020
Db	3961	GCTGCTCCGTGTGGAAATCCAGTGGCGGACCTCGAAGGCTTCTGGGGGAAACATATG	4020
Qy	4021	TGGAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTTGCCACTGCTGCGCAACCC	4080
Db	4021	TGGAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTTGCCACTGCTGCGCAACCC	4080
Qy	4081	CGCATAGCATCATGATGGCATTTACAGCTCTATCACAGCGGCTTACACCCACAT	4140
Db	4081	CGCATAGCATCATGATGGCATTTACAGCTCTATCACAGCGGCTTACACCCACAT	4140
Qy	4141	ACCTTCTGTTTAAACATCTCGGGGGATGGGTGGCGGCCCAACTTTGCTCTCCAGCGCT	4200
Db	4141	ACCTTCTGTTTAAACATCTCGGGGGATGGGTGGCGGCCCAACTTTGCTCTCCAGCGCT	4200
Qy	4201	GCTTCTGCTTTCTGAGGCGCCGCAATCGCTGGAGCGGCTTTGGCAGCATAGGCGCTGG	4260
Db	4201	GCTTCTGCTTTCTGAGGCGCCGCAATCGCTGGAGCGGCTTTGGCAGCATAGGCGCTGG	4260
Qy	4261	AAGGTGCTTGTGGATATTTTGGCAGTTATGGAGCAGGGGTGGCAGCGCTCGTGGCC	4320
Db	4261	AAGGTGCTTGTGGATATTTTGGCAGTTATGGAGCAGGGGTGGCAGCGCTCGTGGCC	4320
Qy	4321	TTTAAAGTTCATGAGCGCGGAGATGCCCTCACCGAGGACCTGTTAACTCTCCCTGCT	4380
Db	4321	TTTAAAGTTCATGAGCGCGGAGATGCCCTCACCGAGGACCTGTTAACTCTCCCTGCT	4380
Qy	4381	ATCTCTTCCCTCGGCGCCCTAGTCTGCGGGGTGGTGGCAGGAGTACTGGTGGGAC	4440
Db	4381	ATCTCTTCCCTCGGCGCCCTAGTCTGCGGGGTGGTGGCAGGAGTACTGGTGGGAC	4440
Qy	4441	GTGGGCGCCAGGGAGGGGCTGTGCAGTGGAGTGAACCGGCTGATAGCGTTGCTTCGCG	4500
Db	4441	GTGGGCGCCAGGGAGGGGCTGTGCAGTGGAGTGAACCGGCTGATAGCGTTGCTTCGCG	4500
Qy	4501	GGTAAACAGCTCTCCCGCCAGGACATATGTGCTGAGAGCGAGCTCAGCAAGTGTCACT	4560
Db	4501	GGTAAACAGCTCTCCCGCCAGGACATATGTGCTGAGAGCGAGCTCAGCAAGTGTCACT	4560
Qy	4561	CAGATCCTCTTCTAGTCTTACCATCACTCAGCTGCTGAAAGGCTTCCAGTGGATCAAC	4620
Db	4561	CAGATCCTCTTCTAGTCTTACCATCACTCAGCTGCTGAAAGGCTTCCAGTGGATCAAC	4620

QY 4621 GAGGACTGCTCCACGCCATGCTCCGGCTGTGGCTAAGAGATCTTTGGGATTGGATATGC 4680
DB 4621 GAGGACTGCTCCACGCCATGCTCCGGCTGTGGCTAAGAGATCTTTGGGATTGGATATGC 4680
QY 4681 ACGGTGTGACTGATTTCAGAGCTCGCTCCAGTCCCAAGCTCTCTGCGCGATTTGCCGGGA 4740
DB 4681 ACGGTGTGACTGATTTCAGAGCTCGCTCCAGTCCCAAGCTCTCTGCGCGATTTGCCGGGA 4740
QY 4741 GTCCCTCTCTTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGCGACGCCATCATG 4800
DB 4741 GTCCCTCTCTTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGCGACGCCATCATG 4800
QY 4801 CAACACACCTGCCATGTGGAGCAGATCAACGGACATGTGAAACACGGTTCCATGAGG 4860
DB 4801 CAACACACCTGCCATGTGGAGCAGATCAACGGACATGTGAAACACGGTTCCATGAGG 4860
QY 4861 ATCGTGGGCTTCCAGTGTAGTAAACGTGCGATGGAACATTTCCCAATTAAACGGGTAC 4920
DB 4861 ATCGTGGGCTTCCAGTGTAGTAAACGTGCGATGGAACATTTCCCAATTAAACGGGTAC 4920
QY 4921 ACCACGGGCTTCCAGTGTAGTAAACGTGCGATGGAACATTTCCCAATTAAACGGGTAC 4980
DB 4921 ACCACGGGCTTCCAGTGTAGTAAACGTGCGATGGAACATTTCCCAATTAAACGGGTAC 4980
QY 4981 GCTGCTGAGGAGTACGTGAGGATAGCGGGTGGGGATTTTCCATCACTGAGCGGCAATG 5040
DB 4981 GCTGCTGAGGAGTACGTGAGGATAGCGGGTGGGGATTTTCCATCACTGAGCGGCAATG 5040
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DB 5041 ACCACTGACAACTGAAAGTCCCGTGTACAGTTCGCGCCCGAATTTCTTACAGAAATG 5100
QY 5101 GATGGGTGGGTGTCACAGGTACGCTCCAGGTGTCACAAACCCCTCTACGGGAGGAGTTC 5160
DB 5101 GATGGGTGGGTGTCACAGGTACGCTCCAGGTGTCACAAACCCCTCTACGGGAGGAGTTC 5160
QY 5161 ACATTCCTGCTGGCTCAATCAATACCTGTTGGGTACAGTCCCAATGCGAGCCGAA 5220
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DB 5221 CCGGACGTAGCAGTCTCACTTCCATGCTACCGACCCCTCCCAATTAACGGCGAGAG 5280
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DB 5401 CTATCAGGCGCAACCTCTCTGCGGAGAGATGCGGAGATGCGGAGGAGGATGAG 5460
QY 5461 TCAGAAATAGGTAGTAAATTTTGGACTCTTTTCAGCGCTTCCAGCGGCTCCAGCGGAGGATGAG 5520
DB 5461 TCAGAAATAGGTAGTAAATTTTGGACTCTTTTCAGCGCTTCCAGCGGCTCCAGCGGAGGATGAG 5520
QY 5521 AGGAGATATCCGTTCCGGCGGAGATCTCGGAGGTCAGGAAATTTCCCTCGAGCGATG 5580
DB 5521 AGGAGATATCCGTTCCGGCGGAGATCTCGGAGGTCAGGAAATTTCCCTCGAGCGATG 5580
QY 5581 CCCATATGGGCGACCCCGGATTAACACCTCCCTGTTAGAGTCTTGAAGGACCCCGGAC 5640
DB 5581 CCCATATGGGCGACCCCGGATTAACACCTCCCTGTTAGAGTCTTGAAGGACCCCGGAC 5640
QY 5641 TAGTCTCCTCAGTGTACAGGGTGTCCATTTGCGGCTGCAAGGCCCTTCCGATACCA 5700
DB 5641 TAGTCTCCTCAGTGTACAGGGTGTCCATTTGCGGCTGCAAGGCCCTTCCGATACCA 5700
QY 5701 CTCCACGGAGGAGAGGACGGTTGCTCTGTCAGAAATCTTACCCTGTCTTCTGCTTTGGCG 5760

DB 5701 CCTCCACGGAGGAGAGGACGGTTGCTGTGAGAATCTACCGTGTCTTCTGCTTTGGCG 5760
QY 5761 GAGTCTCGCCACAAGACCTTTCGCGAGTCCGAATCTCGGCCCTCGACAGCGGCAAGGCA 5820
DB 5761 GAGTCTCGCCACAAGACCTTTCGCGAGTCCGAATCTCGGCCCTCGACAGCGGCAAGGCA 5820
QY 5821 ACGGCTCTCTCTGACACGAGCCCTCCGACGAGCGGAGCCGGGATCCGACGTTGAGTCTGTAC 5880
DB 5821 ACGGCTCTCTCTGACACGAGCCCTCCGACGAGCGGAGCCGGGATCCGACGTTGAGTCTGTAC 5880
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DB 5881 TCTCTCATGCTCCCGCTTTCGAGGCGGAGCCGGGATCCGATCTCTCAGCGACGGGCTTTGG 5940
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DB 5941 TCTACCGTAAGCAGGAGGCTAGTGAAGACGCTGCTGCTGCTCGATGCTTACACATCG 6000
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DB 6001 ACAGGCGCCCTGATCAGCGCATGCGGTGCGGAGGAAACCAAGCTGCCATCAATGACATG 6060
QY 6061 AGCAACTCTTTGCTCCGTCACCAACCTTGTGCTATGCTTACCAATCTCGACGCGCAAGC 6120
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DB 6121 CTGCGGCAAGAGAGTCACTTTGACAGACTGAGGCTCTGAGGAGCCACATPACCGGGAC 6180
QY 6181 GTGCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAAGGCTTAACTTCTATCCGTGGAG 6240
DB 6181 GTGCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAAGGCTTAACTTCTATCCGTGGAG 6240
QY 6241 GAAGCCTGTAAGCTGACGCCGCCACATTCGCGCGAGATCTAAATTTGGCTATGGGCAAG 6300
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DB 6301 GACGTCGGAACTTATCCAGCAAGGCCGTTAAACACATCCGCTCCGTTGGAAGGACTTG 6360
QY 6361 CTGGAAGACACTGAGACACCAATTTGACACCAATTCATGCGCAAAATAGGTTTCTGCG 6420
DB 6361 CTGGAAGACACTGAGACACCAATTTGACACCAATTCATGCGCAAAATAGGTTTCTGCG 6420
QY 6421 GTCCAAACAGAGAGGCGGCGCAAGCGCTTAAACACATCCGCTCCGTTGGAAGGACTTG 6480
DB 6421 GTCCAAACAGAGAGGCGGCGCAAGCGCTTAAACACATCCGCTCCGTTGGAAGGACTTG 6480
QY 6481 GTTGTGTGTGCGAGAAATTTGGGCTTTTACGATGCTTCCACCTCCCTCAGGCGGTG 6540
DB 6481 GTTGTGTGTGCGAGAAATTTGGGCTTTTACGATGCTTCCACCTCCCTCAGGCGGTG 6540
QY 6541 ATGGGCTCTTTCATACGAGTTCCAAATCTCTCTGAGCAGCGGCTCGAGTTCTTGCTGAAT 6600
DB 6541 ATGGGCTCTTTCATACGAGTTCCAAATCTCTCTGAGCAGCGGCTCGAGTTCTTGCTGAAT 6600
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DB 6601 GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGATATGACACCGCTGTTTGTACTCA 6660
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DB 6661 ACGGTCTCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGCTGCTGCTGCC 6720
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DB 6721 CCCGAGCGAGCAGCGCATTAAGTCTGCTCAGAGCGGCTTTTACATCGGGGCCCCCTG 6780
QY 6781 ACTTAATCTTAAAGGCGAGAACTCGCGCTATCCGCTGCGCGAGCGGTGTACTGACG 6840

QY	7921	TAGCTGTGAAAGTCCGTCGAGCGCTTGTACTGTCAGAGAGTGTCTGATCTCTCTGC	7980
Db	7921		7980
QY	7921	TAGCTGTGAAAGTCCGTCGAGCGCTTGTACTGTCAGAGAGTGTCTGATCTCTCTGC <td>7980</td>	7980
Db	7921		7980
QY	7981	AGATCAAGT	7989
Db	7981		7989
QY	7981	AGATCAAGT	7989
Db	7981		7989

Search completed: November 1, 2004, 19:16:14

Job time : 2241 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 05:46:00 ; Search time 21399 Seconds
(without alignments)
17661.539 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagccccgattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sw.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7992	100.0	10690	6	AX739972 Sequence
2	7989	100.0	7989	6	AR406043 Sequence
3	7989	100.0	7989	6	AX036255 Sequence
4	7989	100.0	7989	12	AX242652 Hepatitis
5	7967	99.7	8001	6	AR406042 Sequence
6	7967	99.7	8001	6	AX036254 Sequence
7	7967	99.7	8001	12	SSE242654
8	7949.4	99.5	8001	6	AR406047
9	7949.4	99.5	8001	6	AX036259
10	7947.8	99.4	8001	6	AR406045
11	7947.8	99.4	8001	6	AX036257
12	7941.4	99.4	8001	6	AR406049
13	7941.4	99.4	8001	6	AX036261
14	7611.8	95.2	12305	6	AX937622
15	7608.6	95.2	12315	6	AX937621
16	7331	91.7	8637	6	AR406041
17	7331	91.7	8637	6	AX036253
18	7331	91.7	8637	12	SSE242651
19	7309	91.5	8649	6	AR406044

20	7309	91.5	8649	6	AX036256	AX036256 Sequence
21	7309	91.5	8649	12	SSE242653	AJ242653 Hepatitis
22	7273.8	91.0	8639	6	AR488100	AR488100 Sequence
23	7273.8	91.0	8639	6	AX472291	AX472291 Sequence
24	7272.8	91.0	8638	6	AR488121	AR488121 Sequence
25	7272.8	91.0	8638	6	AX472314	AX472314 Sequence
26	7249.8	90.7	8638	6	AR488105	AR488105 Sequence
27	7249.8	90.7	8638	6	AX472297	AX472297 Sequence
28	7248.8	90.7	8638	6	AR488122	AR488122 Sequence
29	7248.8	90.7	8638	6	AX472315	AX472315 Sequence
30	7246.8	90.7	8642	6	AR488101	AR488101 Sequence
31	7246.8	90.7	8642	6	AX472292	AX472292 Sequence
32	7245.6	90.7	8638	6	AR488104	AR488104 Sequence
33	7245.6	90.7	8638	6	AX472296	AX472296 Sequence
34	7229.8	90.5	8648	6	AR488103	AR488103 Sequence
35	7229.8	90.5	8648	6	AX472295	AX472295 Sequence
36	7222.6	90.4	8643	6	AR488102	AR488102 Sequence
37	7222.6	90.4	8643	6	AX472294	AX472294 Sequence
38	6681.4	83.6	9658	14	AB119282	AB119282 Hepatitis
39	6186.8	77.4	9605	6	AX739971	AX739971 Sequence
40	6186.8	77.4	9605	14	HCJ238799	AJ238799 Hepatitis
41	6186.8	77.4	11076	6	AR406040	AR406040 Sequence
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43	6169.2	77.2	11076	6	AR406048	AR406048 Sequence
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO2059321.
ACCESSION AX739972
VERSION AX739972.1 GI:30519246
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS de Francesco, R., Migliaccio, G. and Paonessa, G.
TITLE Hepatitis C virus replicons and replicon enhanced cells
JOURNAL Patent: WO 02059321-A 3 01-AUG-2002;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)

FEATURES
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VERSION AJ242652.1 GI:5441834
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gene; NS4b protein; NS5a gene; NS5A phosphoprotein; NS5b gene; NS5B
RNA dependant RNA polymerase; polyprotein.
Hepatitis C virus replicon I377/NS3-3'UTR
Hepatitis C virus replicon I377/NS3-3'UTR
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artificial sequences; vectors.
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Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, L. and
Bartschslager, R.
Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell
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Science 285 (5424), 110-113 (1999)
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Direct Submission
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DB	781	CGGTACTCTGCCATTCCACCAACGAGCAACATCGCATCGAGCGAGCAGTACTCGGA 840
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DB	841	TGGAAGCGGCTCTTCTCGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGCGCCAG 900
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DB	901	CCGAATCTGTCCAGGCTCAAGGCGCGCATGCCGACGAGGAGATCTCGTCTGACCC 960
QY	949	ATGGGATGCTGCTTGGCGAATATCATGTTGAAAAATGCGCGCTTTTCTGGATTCAATCG 1008
DB	961	ATGGGATGCTGCTTGGCGAATATCATGTTGAAAAATGCGCGCTTTTCTGGATTCAATCG 1020
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QY	1309	TCCACCATATTGCGCTTCTTGGCAATGAGGCGCGGAAACCTGGCCCTGTCTCTTG 1368
DB	1321	TCCACCATATTGCGCTTCTTGGCAATGAGGCGCGGAAACCTGGCCCTGTCTCTTG 1380
QY	1369	ACGAGCATCTCTAGGGGTCTTCCCTCTGCGCAAGAGATGCAAGTCTGTGTAATGTC 1428
DB	1381	ACGAGCATCTCTAGGGGTCTTCCCTCTGCGCAAGAGATGCAAGTCTGTGTAATGTC 1440
QY	1429	GTGAAGGACAGTCTCTCTGGAAGCTTCTTGAAGCAAAACAACTGTAGGACCCCTT 1488
DB	1441	GTGAAGGACAGTCTCTCTGGAAGCTTCTTGAAGCAAAACAACTGTAGGACCCCTT 1500
QY	1489	TGAGGACGCGGAAACCCCTTGGCGACAGGTGCTCTGCGGCCAAACACGCTGTA 1548
DB	1501	TGAGGACGCGGAAACCCCTTGGCGACAGGTGCTCTGCGGCCAAACACGCTGTA 1560
QY	1549	TAAAGATACCTGCAAAAGCGGACAAACCCAGTGCACCTTGTGAGTTCGATAGTTGTG 1608
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DB	1621	GAAAGTCAAAAGCTCTCTCAAGGCTATTCAAGGGGCTGAAAGATGCCAGAAAG 1680
QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAG 1728
DB	1681	GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAG 1740
QY	1729	TCGAGGTTTAAAAACGCTTAGCCCCCGGACACGCGGACGCTGTTTCTCTTTGAAAAA 1788
DB	1741	TCGAGGTTTAAAAACGCTTAGCCCCCGGACACGCGGACGCTGTTTCTCTTTGAAAAA 1800
QY	1789	CACGATTAATCAATGCGGCTTATTACGCGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1848
DB	1801	CACGATTAATCAATGCGGCTTATTACGCGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1860
QY	1849	TGCATCATCTAGCTTCAAGCGCGGACAGGAACCAAGTTCGAGGGGGAGGTCCAGGTG 1908
DB	1861	TGCATCATCTAGCTTCAAGCGCGGACAGGAACCAAGTTCGAGGGGGAGGTCCAGGTG 1920
QY	1909	GTCTCCACCGCAACCAATCTTCTGCGACCTGCGTCAATGGCGTGTGTTGACTGTC 1968
DB	1921	GTCTCCACCGCAACCAATCTTCTGCGACCTGCGTCAATGGCGTGTGTTGACTGTC 1980
QY	1969	TATCATGTGCGGCTCAAAAGACCTTTCGCCGCCCCAAAGGCCCAATCACCCAAATGTAC 2028
DB	1981	TATCATGTGCGGCTCAAAAGACCTTTCGCCGCCCCAAAGGCCCAATCACCCAAATGTAC 2040

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Dd	4261	ATAGGCTTTGGAAAGGTGCTTGTGGATATTTTGGGAGGTTATGGACAGGGGTGGCAGGC	4320
Qy	4309	GGCTGCTGGCCTTTAAAGTCATGAGCGGAGATCCCTCCACAGGACCTGTTTAAAC	4368
Dd	4321	GGCTGCTGGCCTTTAAAGTCATGAGCGGAGATCCCTCCACAGGACCTGTTTAAAC	4380
Qy	4369	CTACTCCCTGCTATCTCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGGCGAGGATA	4428
Dd	4381	CTACTCCCTGCTATCTCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGGCGAGGATA	4440
Qy	4429	CTGCTGGGCACTGCGGCGGAGGGGAGGGGCTGTGCGATGATGAACCGGCTGATAGCG	4488
Dd	4441	CTGCTGGGCACTGCGGCGGAGGGGAGGGGCTGTGCGATGATGAACCGGCTGATAGCG	4500
Qy	4489	TTGCTGCGGGGATTAACACAGCTCTCCCGCACGCTATGTGCTGAGAGCGAGCTGCA	4548
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Qy	4549	GCAAGCTGCTACTCAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGCTTCAC	4608
Dd	4561	GCAAGCTGCTACTCAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGCTTCAC	4620
Qy	4609	CAGTGGATCAACAGAGACTGCTCCACGCACTGCTCCGGCTGCTGGCTAAGAGATGTTGG	4668
Dd	4621	CAGTGGATCAACAGAGACTGCTCCACGCACTGCTCCGGCTGCTGGCTAAGAGATGTTGG	4680
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Dd	4921	ATTAAAGGCTACACACGGGCGCTGCAAGCTTCCCGCGGCGCAAAATTAATTCAGGGCG	4980
Qy	4969	CTGTGGCGGGTGGCTGTGAGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAC	5028
Dd	4981	CTGTGGCGGGTGGCTGTGAGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAC	5040
Qy	5029	GTGACGGCATGACCACTGACAACTGTAAGTCCCGTGTCAAGTTCCCGGCGCGCAATTC	5088
Dd	5041	GTGACGGCATGACCACTGACAACTGTAAGTCCCGTGTCAAGTTCCCGGCGCGCAATTC	5100
Qy	5089	TTTACAGAGTGGATGGGGTGGGTTGCAAGGTACGTCCAGGTGCAACCCCTCTTA	5148
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Dd	5161	CGGGAGGAGTCAATCTGCTGGGCTCAATCAATACCTGTTGGGTTCACAGCTCCCA	5220
Qy	5209	TGCGAGCCGAAACCGGACGTAGCAGTCTCACTTCCATGCTCAACGACCCCTCCACAT	5268
Dd	5221	TGCGAGCCGAAACCGGACGTAGCAGTCTCACTTCCATGCTCAACGACCCCTCCACAT	5280
Qy	5269	ACGGGAGGACGGCTAAGCTGAGCTGGCGAGGGATCTCCCGCTTCTGGCGAGCTCA	5328
Dd	5281	ACGGGAGGACGGCTAAGCTGAGCTGGCGAGGGATCTCCCGCTTCTGGCGAGCTCA	5340
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Dd	5341	TCAGCTAGCCAGCTGTGCGGCTTCTTGAAGGCAATGCACTACCGCTCATGACTCC	5400
Qy	5389	CGGAGCGTGAATCATGAGGCGACCTCTGCTGGCGAGAGATGGCGGGAACATC	5448
Dd	5401	CGGAGCGTGAATCATGAGGCGACCTCTGCTGGCGAGAGATGGCGGGAACATC	5460
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Dd	5461	ACCGCGTGGAGTCAGAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAGCG	5520
Qy	5509	GAGGAGATGAGAGGAGATATCCGTTCCGCGGAGATCTCGCGAGGTCCAGGAAATTC	5568
Dd	5521	GAGGAGATGAGAGGAGATATCCGTTCCGCGGAGATCTCGCGAGGTCCAGGAAATTC	5580
Qy	5569	CTTCGAGCGATGCGGATATGGGCAACCGGATTAACCCCTCCACTGTTTGAAGTCTCTGG	5628
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DEFINITION Sequence 3 from Patent EP1043399.
ACCESSION AX036254
VERSION AX036254.1 GI:11225870
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SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 3 11-OCT-2000;
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Db 1621 GAAAGAGTCAAAATGGCTCTCTCAAGCTATTCAACAAAGGGCTGAAGGATGCCGAAG 1680
Qy 1669 GTACCCATTTGATGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTATG 1728
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Qy 1729 TCCAGGTTTAAAAAAGCTTAGGCCCCCGCAACCAAGGGACGTGTTTCTTTGAAAAA 1788
Db 1741 TCCAGGTTTAAAAAAGCTTAGGCCCCCGCAACCAAGGGACGTGTTTCTTTGAAAAA 1800
Qy 1789 CACGATAATACCATGGCGCTATTACGGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1848
Db 1801 CACGATAATACCATGGCGCTATTACGGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1860
Qy 1849 TGCATCATCTAGCTCTCAGCGCGGACAGGAACCAAGTTCAGAGGGAGGTCACAGTG 1908
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Qy 1909 GTCTCCACCGCAACAAATCTTCTCGCGACCTGCTCAATGCGCTGTGTGACTGTC 1968
Db 1921 GTCTCCACCGCAACAAATCTTCTCGCGACCTGCTCAATGCGCTGTGTGACTGTC 1980
Qy 1969 TATCATGCTGCGCTCAAAAGACCTTTGCGGCCCCAAAGGGCCCCAATCACCCAAATGTAC 2028
Db 1981 TATCATGCTGCGCTCAAAAGACCTTTGCGGCCCCAAAGGGCCCCAATCACCCAAATGTAC 2040
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Qy 2089 CCATGCACTGCGGAGCTCGGACCTTTACTTGTGTACAGAGGATGCCGATGTCAATCCG 2148
Db 2101 CCATGCACTGCGGAGCTCGGACCTTTACTTGTGTACAGAGGATGCCGATGTCAATCCG 2160
Qy 2149 GTGCGCGGCGGCGGACAGCAGCGGGGAGCTTACTTCTCCCGCAGGCCGCTTCTTACTTG 2208
Db 2161 GTGCGCGGCGGCGGCGACAGCAGAGGGGAGCTTACTTCTCCCGCAGGCCGCTTCTTACTTG 2220
Qy 2209 AAGGGCTTCTCGGGGTCACCTGCTGCGGCGGACGCTGTGGGCACTTTTCGG 2268
Db 2221 AAGGGCTTCTCGGGGTCACCTGCTGCGGCGGACGCTGTGGGCACTTTTCGG 2280
Qy 2269 GCTGCGGTGTGACCCCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGGTGAGTCTATG 2328
Db 2281 GCTGCGGTGTGACCCCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGGTGAGTCTATG 2340

QY 2329 GAAACCACTATCGGGTCCCGGCTTTACGGACAACCTCTGTCCTCCCTCCCGCCGCTACCGCAG 2388
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QY 2389 ACATTCACAGTGGCCCATCTACACGCCCTACTGCTAGCGGCAAGACACTAAGTGGCG 2448
DB 2401 ACATTCACAGTGGCCCATCTACACGCCCTACTGCTAGCGGCAAGACACTAAGTGGCG 2460
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DB 2461 GCTCGTATGCAACCCAAAGGTTAAGGTGCTTGTCTGAAACCCCTCGCTCCCGCCAC 2520
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DB 2521 CTAGGTTTCGGGCGGTATATGCTTAAGGACATGATGATCGACCCCTAAACATCAAGAACCGGG 2580
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DB 2581 GTAAGGACCATCACACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTCTTCC 2640
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DB 2821 ATCGAGAGGTGCTCTGTCAGCACTCGGAGAAATCCCTTTTATGGCAAGCCATCCCC 2880
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DB 3301 GAGCGGGCTGTGCTTGTGATGAGCTCACGCCGCGAGACCTCAGTTAGTTTTCGGGCT 3360
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DB 3361 TACCTAAACACAACAGGGTTGCCGCTTGCACGACCATCTGGAGTTCTGGGAGAGCGTC 3420
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DB 3421 TTTACAGCCCTCACCCNACATAGAGGCCCATTTCTTGTCCAGACTAAGACGAGGAGAGAC 3480
QY 3469 AACTTCCCTTACTCTGGTAGCATACAGGCTACGGTGTGCGCCAGGAGCTCAGGCTCCACCT 3528
DB 3481 AACTTCCCTTACTCTGGTAGCATACAGGCTACGGTGTGCGCCAGGAGCTCAGGCTCCACCT 3540
QY 3529 CCATCGTGGGACCAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGGCCA 3588
DB 3541 CCATCGTGGGACCAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGGCCA 3600
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DB 3601 AGCCCTCTGCTGTATAGGCTGGAGCCGTTCAAAACGAGGTTACTACACACACCCCATATA 3660
QY 3649 ACCAAATACATCATGCGATGCGATGCGCTGACCTGGAGGTGCTCAGGACACCTGGGTG 3708
DB 3661 ACCAAATACATCATGCGATGCGATGCGCTGACCTGGAGGTGCTCAGGACACCTGGGTG 3720
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QY 3769 ATTGTGGSCAGGATCATCTTGTCCGGAAGCCGCGCATCATTTCCCGACAGGAGTCTT 3828
DB 3781 ATTGTGGSCAGGATCATCTTGTCCGGAAGCCGCGCATCATTTCCCGACAGGAGTCTT 3840
QY 3829 TACCGGAGTTCGATGAGATGCGCTCAGACCTCCCTTACATCGAACAGGGA 3888
DB 3841 TACCGGAGTTCGATGAGATGCGCTCAGACCTCCCTTACATCGAACAGGGA 3900
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DB 3901 ATGAGCTCGCGCAACAAATTCAPACAGAGCAATCGGTTGCTGCAACAGCCACCAAG 3960
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DB 3961 CAAGCGAGGCTGCTGCTCCGCTGGAATTCAGTGGCGACCTCGAAGCCTTCTGG 4020
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DB 4021 GCGAAGCATATGTGGAAATTTATCAGCGGGATACAAATTTAGCAGGCTTCTCCACTCTG 4080
QY 4069 CTTGGCAACCCCGGATAGCATCATCTATGCGATTCACAGCTCTATCACAGCCCGCTC 4128
DB 4081 CTTGGCAACCCCGGATAGCATCATCTATGCGATTCACAGCTCTATCACAGCCCGCTC 4140
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DB 4261 ATAGGCTCTGGGAAGTGTGTTGGATATTTTGGCAGGTTATGGAGCAGGCTGGCAGGC 4320
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QY 4429 CTTGCTCGCAGCTGGGCGGAGGAGGCTGTCAGTGGATGAACCGGCTGATAGCG 4488
DB 4441 CTTGCTCGCAGCTGGGCGGAGGAGGCTGTCAGTGGATGAACCGGCTGATAGCG 4500
QY 4489 TTTGCTTCGCGGGGTAACCAAGCTCTCCCGCACCATATGCTGCTGAGACGAGCTGCA 4548

4501	Db	TTCCGTTCCGGGGTAAACAAGTCTCCCCACGCACTATGTGCTCGAGAGCGACGCTGCA	4560
4549	Qy	GCACGTGCTCACTCAGATCCTCTCTAGTCTTTACCATCACTCAGCTGCTGAAGAGCTTCAAC	4608
4561	Db	GCACGTGTCACTCAGATCCTCTCTAGTCTTACCACTCACTCAGCTGCTGAAGAGCTTCAC	4620
4609	Qy	CAGTGGATCAACAGAGGATGCTCCACGCCATGCTCGGCTCGTGGCTAAGAGATGTTTGG	4668
4621	Db	CAGTGGATCAACAGAGGATGCTCCACGCCATGCTCGGCTCGTGGCTAAGAGATGTTTGG	4680
4669	Qy	GATTGGATATGCAAGGTGTGATGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCTCTGCGG	4728
4681	Db	GATTGGATATGCAAGGTGTGATGATTTTCAAGACCTGGCTCCAGTCCAAAGCTCTCTGCGG	4740
4729	Qy	CGATTGCCGGAGTCCCTTCTCTCATGTCAAAGTGGGTCAAGAGGAGTCTGGCGGGGC	4788
4741	Db	CGATTGCCGGAGTCCCTTCTCTCATGTCAAAGTGGGTCAAGAGGAGTCTGGCGGGGC	4800
4789	Qy	GACGGCATCATGCAAAACAACCTGGCCATGTGGAGCACAGATCACCGGACATGTGAAAAC	4848
4801	Db	GACGGCATCATGCAAAACAACCTGGCCATGTGGAGCACAGATCACCGGACATGTGAAAAC	4860
4849	Qy	GGTTCCATAGGATCGTGGGCGCTAGGACCTGTAGTAAACAAGTGGCATGGAACATTTCCC	4908
4861	Db	GGTTCCATAGGATCGTGGGCGCTAGGACCTGTAGTAAACAAGTGGCATGGAACATTTCCC	4920
4909	Qy	ATTAAACGGTACACACAGGGGCCCCGTGCACGCCCTCCCGCGCGCAAAATTTCTAGGGCG	4968
4921	Db	ATTAAACGGTACACACAGGGGCCCCGTGCACGCCCTCCCGCGCGCAAAATTTCTAGGGCG	4980
4969	Qy	CTGTGGCGGGTGGCTGTGAGGAGTACGTGGAGGTTACCGGGGTGGGGGATTTCCACTAC	5028
4981	Db	CTGTGGCGGGTGGCTGTGAGGAGTACGTGGAGGTTACCGGGGTGGGGGATTTCCACTAC	5040
5029	Qy	GTGACGGGCATGACCATGACAAAGTAAAGTGCCTGTACAGTTCGGGCCCCCGAAATTC	5088
5041	Db	GTGACGGGCATGACCATGACAAAGTAAAGTGCCTGTACAGTTCGGGCCCCCGAAATTC	5100
5089	Qy	TTTCAACAAGTGGATGGGGTCCGGTGTGCACAGGTACGCTCACGGTGCAAAACCCCTCTTA	5148
5101	Db	TTTCAACAAGTGGATGGGGTCCGGTGTGCACAGGTACGCTCACGGTGCAAAACCCCTCTTA	5160
5149	Qy	CGGGAGAGGTACATTCCTCGTGGGTCAATCAATACCTGGTTGGGTCAAGCTTCCA	5208
5161	Db	CGGGAGAGGTACATTCCTCGTGGGTCAATCAATACCTGGTTGGGTCAAGCTTCCA	5220
5209	Qy	TGCGAGCCGGAACCGGAGTACAGTGTCACTTCCATGTCTCACCGACCCCTCCCAAT	5268
5221	Db	TGCGAGCCGGAACCGGAGTACAGTGTCACTTCCATGTCTCACCGACCCCTCCCAAT	5280
5269	Qy	ACGGCGGAGACGGCTAAGCTAGGTGGCCACAGGGATCTCCCCCTCTTTGGCCAGCTCA	5328
5281	Db	ACGGCGGAGACGGCTAAGCTAGGTGGCCACAGGGATCTCCCCCTCTTTGGCCAGCTCA	5340
5329	Qy	TCAGCTAGCCAGCTGTCTGGCGCTTCCTTTGAAGGCAACATGCACATCCCGTCAATGCTCC	5388
5341	Db	TCAGCTAGCCAGCTGTCTGGCGCTTCCTTTGAAGGCAACATGCACATCCCGTCAATGCTCC	5400
5389	Qy	CCGGACGTGACCTCATCGAGGCCAACCTCTCTGTGGCGGACAGGATGGCGCGGAACATC	5448
5401	Db	CCGGACGTGACCTCATCGAGGCCAACCTCTCTGTGGCGGACAGGATGGCGCGGAACATC	5460
5449	Qy	ACCCGGTGGAGTCAGAAAATTAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5508
5461	Db	ACCCGGTGGAGTCAGAAAATTAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5520
5509	Qy	GAGGAGGATGAGGGGAATNTCCGTTCCGGCGGAGATCTCTGGCGGAGTCCAGGAAATTC	5568
5521	Db	GAGGAGGATGAGGGGAATNTCCGTTCCGGCGGAGATCTCTGGCGGAGTCCAGGAAATTC	5580
5569	Qy	CCTCGAGCGATGCCCATATATGGGACGCCCGGATTAACAACCTCTTGTAGAGTCTCTGG	5628
5581	Db	CCTCGAGCGATGCCCATATATGGGACGCCCGGATTAACAACCTCTTGTAGAGTCTCTGG	5640

QY	5629	AAGGA	CCCGGACTACGTCCTCCAGTGGGTACACGGGTGTCCATTCCGCCCTGCCAAGGCC	5688
DB	5641	AAGGA	CCCGGACTACGTCCTCCAGTGGGTACACGGGTGTCCATTCCGCCCTGCCAAGGCC	5700
QY	5689	CCTCCGATACCACTCCACGGAGGAAGAGACGGTGTCTGTACAGAAATCTACCGTGTCT	5748	
DB	5701	CCTCCGATACCACTCCACGGAGGAAGAGACGGTGTCTGTACAGAAATCTACCGTGTCT	5760	
QY	5749	TCGTGCTTTGGCGAGCTCGGCACAAAGACCTTTCGGCAGCTCCGATCTCGCGCGCTCGAC	5808	
DB	5761	TCGTGCTTTGGCGAGCTCGGCACAAAGACCTTTCGGCAGCTCCGAAATCTGTGCGCGCTCGAC	5820	
QY	5809	AGCGGCACGCAACGGCTCTCTCTGACACAGCCCTCCGACGACGGCGGATCCGAC	5868	
DB	5821	AGCGGCACGCAACGGCTCTCTCTGACACAGCCCTCCGACGACGGCGGATCCGAC	5880	
QY	5869	GTTGAGTCGTACTCTTCATGCGCCCCCTTTGAGGGGGAGCGGGGATCCCGATCTCAGC	5928	
DB	5881	GTTGAGTCGTACTCTTCATGCGCCCCCTTTGAGGGGGAGCGGGGATCCCGATCTCAGC	5944	
QY	5929	GACGGGCTTTGGTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTGCTCTGCTGCTCGATG	5988	
DB	5941	GACGGGCTTTGGTCTACCGTAAGCGAGGAGGCTAGTGAGGACGTGCTCTGCTGCTCGATG	6000	
QY	5989	TCCTTACATATGGA	CAGCGCGCCCTGATCAGCCCATGCGCTTCGGAGGAGAAACCAAGCTGCGCC	6048
DB	6001	TCCTTACATATGGA	CAGCGCGCCCTGATCAGCCCATGCGCTTCGGAGGAGAAACCAAGCTGCGCC	6060
QY	6049	ATCAATGGA	CTGAGCAACTCTTTGCTTCGTCACCAAACTTGGTCTATGCTACTACACATCT	6108
DB	6061	ATCAATGGA	CTGAGCAACTCTTTGCTTCGTCACCAAACTTGGTCTATGCTACTACACATCT	6120
QY	6109	CGCAGCGCAAGCCTTCGGCGAGAGAGGCTCACCTTTGACAGACTGCAGGTCTCTGGACGAC	6168	
DB	6121	CGCAGCGCAAGCCTTCGGCGAGAGAGGCTCACCTTTGACAGACTGCAGGTCTCTGGACGAC	6180	
QY	6169	CACCTACCGGGACGTGCTCAAGGAGATGAAGCGGAGAGCGGTCACAGTTAAGGCTAACTT	6228	
DB	6181	CACCTACCGGGACGTGCTCAAGGAGATGAAGCGGAGAGCGGTCACAGTTAAGGCTAACTT	6240	
QY	6229	CTATCCGTTGGAGGAAGCCTGTATGCTCAGCCGCCACATTCGCGCCAGATCTAAATTTGGC	6288	
DB	6241	CTATCCGTTGGAGGAAGCCTGTATGCTCAGCCGCCACATTCGCGCCAGATCTAAATTTGGC	6300	
QY	6289	TATGGGGCAAAAGGACGTCCGAAACCTATCCAGCAAGGCGGTTAACCAATCCGCTCCGTG	6348	
DB	6301	TATGGGGCAAAAGGACGTCCGAAACCTATCCAGCAAGGCGGTTAACCAATCCGCTCCGTG	6360	
QY	6349	TGGAAGGACTTCTGGAGAGACATGAGACACCAATTGACACCCATCATCGGCAAAAAT	6408	
DB	6361	TGGAAGGACTTCTGGAGAGACATGAGACACCAATTGACACCCATCATCGGCAAAAAT	6420	
QY	6409	GAGGTTTTCTCGTCCAAACAGAGAAGGGGGCGCAAGCGAGTCCCTTTATCGTATTC	6468	
DB	6421	GAGGTTTTCTCGTCCAAACAGAGAAGGGGGCGCAAGCGAGTCCCTTTATCGTATTC	6480	
QY	6469	CCAGATTTGGGGGTTGTTGTGCGAGAAATGCGCCCTTTACGATGFGTCTCCACCCCTC	6528	
DB	6481	CCAGATTTGGGGGTTGTTGTGCGAGAAATGCGCCCTTTACGATGFGTCTCCACCCCTC	6540	
QY	6529	CCTCAGGGCGTACGGGCTTTCTATACGGATTTCCAAATCTCTCCTGGACAGCGGGTCGAG	6588	
DB	6541	CCTCAGGGCGTACGGGCTTTCTATACGGATTTCCAAATCTCTCCTGGACAGCGGGTCGAG	6600	
QY	6589	TTCTCTGGTGAATGCTTGGAAAACGGAAGAAATGCCCTATGGGCTTCGCAATGACACCCGC	6648	
DB	6601	TTCTCTGGTGAATGCTTGGAAAACGGAAGAAATGCCCTATGGGCTTCGCAATGACACCCGC	6660	
QY	6649	TGTTTTGACTCAACCGTCACTGAGAAATGACATCCGTGTTGAGGAGTCAATCTACCAATGT	6708	
DB	6661	TGTTTTGACTCAACCGTCACTGAGAAATGACATCCGTGTTGAGGAGTCAATCTACCAATGT	6720	

Db 961 ATGGCGATGCTGCTTGGCCGAATATCATGGTGAAAATGSCCGCTTTTCTGGATTCATCG 1020
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Db 1021 ACTGTGGCCGGCTGGGTGTGGCGGACCGGTATCAGGACATAGCGTTGGCTACCCGCGATA 1080
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QY 1909 GTCTCCAACGCAACATCTTTCTGGGACCTTGGCTCAATGGCGTGTGTTGACCTGTC 1968
Db 1921 GTCTCCAACGCAACATCTTTCTGGGACCTTGGCTCAATGGCGTGTGTTGACCTGTC 1980
QY 1969 TATCATGGTGGCGCTCAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCCAAATGTAC 2028
Db 1981 TATCATGGTGGCGCTCAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCCAAATGTAC 2040
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Db 2041 ACCAATGTGACGAGGACCTTCGTGGCTGGCAAGCGCCCCCGGGGCGGCTTCTTGACA 2100
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Db 2761 CGACTCGTCTGCTCGCACCGCTACCGCTCCGGGATCGGTACCCGTCACATCCAAAC 2820
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QY 2869 ATCGAGACCATCAAGGGGGGAGCGACCTCATTTCTGCCATTCCTCAAGAGAAATGTGAT 2928
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QY 2929 GAGTCTCGCCCGAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGCTTT 2988
Db 2941 GAGTCTCGCCCGAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGCTTT 3000
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Db 3061 ACCGGCTTTACCGGCGATTTCCGATCAGTGTGATGCAATACATGTGTACCCAGACA 3120
QY 3109 GTGACTTCAGCTGAGCCCGACCTTTCACCATTTGACGAGCGGCGGTGCGCAGAGCGG 3168
Db 3121 GTGACTTCAGCTGAGCCCGACCTTTCACCATTTGACGAGCGGCGGTGCGCAGAGCGG 3180

Qy	3169	GTGTCAAGCTCGACGCGGAGGACGACATGGTAGGGGACGAGATGGGCAATTTACAGTTT	3228	Qy	4249	ATAGCCCTTGGAAAGGTGCTTGTGGATATTTTGGCAGTTATGGACGAGGGTGGCAGGC	4308
Db	3181	GTGTCAAGCTCGACGCGGAGGACGACATGGTAGGGGACGAGATGGGCAATTTACAGTTT	3240	Db	4261	ATAGCCCTTGGAAAGGTGCTTGTGGATATTTTGGCAGTTATGGACGAGGGTGGCAGGC	4320
Qy	3229	GTGACTCCAGGAGAACGGCCCTGGGCAATGTTTGGATTCCTCGGTTCTGTGCGAGTGCAT	3288	Qy	4309	CGCTCGTGGCCCTTTAAGTTCATGACGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC	4368
Db	3241	GTGACTCCAGGAGAACGGCCCTGGGCAATGTTTGGATTCCTCGGTTCTGTGCGAGTGCAT	3300	Db	4321	CGCTCGTGGCCCTTTAAGTTCATGACGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC	4380
Qy	3289	GACCGGGCTGTGCTTGGTACGAGCTCACGCCCGCCGAGACCTCAGTTAGTTTGGGGCT	3348	Qy	4369	CTACTCCCTGTANTCTCTCCCTGGCGCCCTAGTCTCGGGGTCTGTGTGCGAGCGATA	4428
Db	3301	GACCGGGCTGTGCTTGGTACGAGCTCACGCCCGCCGAGACCTCAGTTAGTTTGGGGCT	3360	Db	4381	CTACTCCCTGTANTCTCTCTCCCTGGCGCCCTAGTCTCGGGGTCTGTGTGCGAGCGATA	4440
Qy	3349	TACCTAAACACACACAGGGTTGCCGTCTGCCAGGACCATGTGAGTCTTGGGAGAGGTC	3408	Qy	4429	CTGCGTCGCGCACGTGGGCCACAGGGAGGGGCTGTGCAGTGGATGAAACCGCGCTGATAGCG	4488
Db	3361	TACCTAAACACACACAGGGTTGCCGTCTGCCAGGACCATGTGAGTCTTGGGAGAGGTC	3420	Db	4441	CTGCGTCGCGCACGTGGGCCACAGGGAGGGGCTGTGCAGTGGATGAAACCGCGCTGATAGCG	4500
Qy	3409	TTTACAGGCTCACCCATAGACGCCCATTTCTTGTCCGAGCTAAGCAGGACGAGAGAC	3468	Qy	4489	TTTTCGCTTCGCGGGTAACACAGTCTCCCCACGACACTATGTGCCTGAGAGCGAGCTGCA	4548
Db	3421	TTTACAGGCTCACCCATAGACGCCCATTTCTTGTCCGAGCTAAGCAGGACGAGAGAC	3480	Db	4501	TTTTCGCTTCGCGGGTAACACAGTCTCCCCACGACACTATGTGCCTGAGAGCGAGCTGCA	4560
Qy	3469	AACTTCCCTTACCTGGTAGCATACAGGCTACGGTGTGGCCAGGGCTCAGGCTCCACCT	3528	Qy	4549	GCACTGTCTCACTCAGATCCTCTTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTTCAC	4608
Db	3481	AACTTCCCTTACCTGGTAGCATACAGGCTACGGTGTGGCCAGGGCTCAGGCTCCACCT	3540	Db	4561	GCACTGTCTCACTCAGATCCTCTCTTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTTCAC	4620
Qy	3529	CCATCGTGGGACCAAAATGTGGAAGTGTCTCATACGGCTTAAAGCCCTACGCTGCA	3588	Qy	4609	CAGTGGATCAACGAGGACTGCTCCACGCCATGCTCCCGGCTCGTGGCTTAAGAGATGTTTG	4668
Db	3541	CCATCGTGGGACCAAAATGTGGAAGTGTCTCATACGGCTTAAAGCCCTACGCTGCA	3600	Db	4621	CAGTGGATCAACGAGGACTGCTCCACGCCATGCTCCCGGCTCGTGGCTTAAGAGATGTTTG	4680
Qy	3589	ACGCCCTGTGTATAGCTGGGAGCCGTTCAAAACAGAGTTACTACACACACCCATA	3648	Qy	4669	GAATTGATATGACCGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCCAAGCTCTCTGCGG	4728
Db	3601	ACGCCCTGTGTATAGCTGGGAGCCGTTCAAAACAGAGTTACTACACACACCCATA	3660	Db	4681	GAATTGATATGACCGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCCAAGCTCTCTGCGG	4740
Qy	3649	ACCAAATACATATGGCATATGTCGTGCGCTGACCTGGAGTGTCTCACAGACCTCGGGT	3708	Qy	4729	CGATTGCCGGAGTCCCTTCTTCTCATGTCAACGTGGGTCAAGGGAGTCTGGCGGGG	4788
Db	3661	ACCAAATACATATGGCATATGTCGTGCGCTGACCTGGAGTGTCTCACAGACCTCGGGT	3720	Db	4741	CGATTGCCGGAGTCCCTTCTTCTCATGTCAACGTGGGTCAAGGGAGTCTGGCGGGG	4800
Qy	3709	CTGTAGGCGGAGTCTTACAGCTCTGGCCGGTATTCGCTGACAAAGCAGCGTGGTC	3768	Qy	4789	GACGGCATATGACAAACACACCTGCCATGTGGAGCACAGATCACCGGACATGTGAAAC	4848
Db	3721	CTGTAGGCGGAGTCTTACAGCTCTGGCCGGTATTCGCTGACAAAGCAGCGTGGTC	3780	Db	4801	GACGGCATATGACAAACACACCTGCCATGTGGAGCACAGATCACCGGACATGTGAAAC	4860
Qy	3769	ATTGTGGGAGGATCATCTTGTCCGGAAGCCGGCCATCTCCGACAGGAGATCCTT	3828	Qy	4849	GGTTCCATGAGGATCTGGGGCTTAGGACCTGTAGTATACAGTGCATGGAACATTTCCC	4908
Db	3781	ATTGTGGGAGGATCATCTTGTCCGGAAGCCGGCCATCTCCGACAGGAGATCCTT	3840	Db	4861	GGTTCCATGAGGATCTGGGGCTTAGGACCTGTAGTATACAGTGCATGGAACATTTCCC	4920
Qy	3829	TACCGGAGTTCGATGAGATGGAAGTGCCTCACACCTCCCTTACATCGAACAGGGA	3888	Qy	4909	ATTAAACGCTTACACACGCGCCCTTGACGCCCTCCCGCGGCCAAATTTATTCTAGGGG	4968
Db	3841	TACCGGAGTTCGATGAGATGGAAGTGCCTCACACCTCCCTTACATCGAACAGGGA	3900	Db	4921	ATTAAACGCTTACACACGCGCCCTTGACGCCCTCCCGCGGCCAAATTTATTCTAGGGG	4980
Qy	3889	ATGACGCTCGCCGAAACAAATTCAAACAGAGGCAATCGGGTGTCTGAAACAGCACCAAG	3948	Qy	4969	CTGTGGCGGTGCTGCTGAGGAGTACGTGAGGTTACGCGGGTGGGGATTTCCACTAC	5028
Db	3901	ATGACGCTCGCCGAAACAAATTCAAACAGAGGCAATCGGGTGTCTGAAACAGCACCAAG	3960	Db	4981	CTGTGGCGGTGCTGCTGAGGAGTACGTGAGGTTACGCGGGTGGGGATTTCCACTAC	5040
Qy	3949	CAAGCGGAGCTGCTCTCGGTGTGGAATCCAGTGGCGGACCTCGAAGCTTCTGG	4008	Qy	5029	GTGACGGGCATGACCACTGACCAAGTAAAGTGCCTGTGAGTTCGCGCCCGCAATTC	5088
Db	3961	CAAGCGGAGCTGCTCTCGGTGTGGAATCCAGTGGCGGACCTCGAAGCTTCTGG	4020	Db	5041	GTGACGGGCATGACCACTGACCAAGTAAAGTGCCTGTGAGTTCGCGCCCGCAATTC	5100
Qy	4009	GCGAGCATATGGAATTTTCATCGCGGATACAAATATTTAGCGGCTTGTCCACTCTG	4068	Qy	5089	TTTCAAGAACTGTGAGGTGGGTGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTTA	5148
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Qy	4129	ACCAACCAATACCTCTGTTTAAATCTCTGGGGATGGGTGGCCGCCAATTTGCT	4188	Qy	5209	TGCGAGCCCGMAACGAGAGTACAGTGTCTCATTCCATGTCTACCGACCTCTCCACATT	5268
Db	4141	ACCAACCAATACCTCTGTTTAAATCTCTGGGGATGGGTGGCCGCCAATTTGCT	4200	Db	5221	TGCGAGCCCGMAACGAGAGTACAGTGTCTCATTCCATGTCTACCGACCTCTCCACATT	5280
Qy	4189	CCTCCAGCGCTGTCTGTCTTCTAGGCGCCGGCATCGCTGGAGCGGTGTGTGCGAG	4248	Qy	5269	ACGCGGAGGACGCGCTAAGCGCTTAGGCTGGCCAGGGGATCTCCCCCTCTTGTGGCCAGCTCA	5328
Db	4201	CCTCCAGCGCTGTCTGTCTTCTAGGCGCCGGCATCGCTGGAGCGGTGTGTGCGAG	4260	Db	5281	ACGCGGAGGACGCGCTAAGCGCTTAGGCTGGCCAGGGGATCTCCCCCTCTTGTGGCCAGCTCA	5340
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Db 3721 CTGTTAGGCGGAGTCTTAGAGCTCTGGCGCGTATTTGCTGACACACGACGCTGGTC 3780
Qy 3769 ATTGTGGCAGGATCATCTTGTCCGAAAGCGGCCATCATTTCCGACAGGGAAGTCCCTT 3828
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Db 3961 CAAGCGGAGCTGTGCTCCGCTGGTGAATCCAAGTGGCGGACCTCGAAGCTTCTGG 4020
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Db 4021 GCGAAGCATATGTGGAATTTTCATCAGCGGGATACAAATTTTAGCAGGCTTTGTCACTG 4080
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Db 4081 CTTGGCAACCCCGATAGCATCTGANTGCAATTCAGGCTCTATCACCAGCCGCTC 4140
Qy 4129 ACACCCCAACATACCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCACTTGCT 4188
Db 4141 ACCACCCCAACATACCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCACTTGCT 4200
Qy 4189 CTTCCAGCGTCTGCTTCTGCTTTTGTAGGCGCCGCGCATCGCTGGAGCGGCTGTTGGCAGC 4248
Db 4201 CTTCCAGCGTCTGCTTCTGCTTTTGTAGGCGCCGCGCATCGCTGGAGCGGCTGTTGGCAGC 4260
Qy 4249 ATAGGCTTTGGGAAGTCTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGC 4308
Db 4261 ATAGGCTTTGGGAAGTCTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGC 4320
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Qy 4429 CTGCTCTGGCAGTGGGCCAGGGAGGGGCTGTGAGTGATGAACCGGCTGATAGC 4488
Db 4441 CTGCTCTGGCAGTGGGCCAGGGAGGGGCTGTGAGTGATGAACCGGCTGATAGC 4500
Qy 4489 TTTGCTCTGGCGGGTTAAACACAGTCTCCCCCAAGCACTATGTGCTGAGAGCGACGTGCA 4548
Db 4501 TTTGCTCTGGCGGGTTAAACACAGTCTCCCCCAAGCACTATGTGCTGAGAGCGACGTGCA 4560
Qy 4549 GCACGTGTCACTCAGATCCTCTAGTCTTACATCAGTCTGAGAGGCTTAC 4608
Db 4561 GCACGTGTCACTCAGATCCTCTAGTCTTACATCAGTCTGAGAGGCTTAC 4620

Qy 4609 CAGTGGATCAACGAGGACTGTCTCAACGCCATGTCTCCGGTCTGTGGCTAAGAGATGTTGG 4668
Db 4621 CAGTGGATCAACGAGGACTGTCTCAACGCCATGTCTCCGGTCTGTGGCTAAGAGATGTTGG 4680
Qy 4669 GATTTGGATATGACCGGTGTTGACTGATTTCAAGACTCTGCTCCAGTCCAAGCTCTCTGGC 4728
Db 4681 GATTTGGATATGACCGGTGTTGACTGATTTCAAGACTCTGCTCCAGTCCAAGCTCTCTGGC 4740
Qy 4729 CGATTTCCGGGAGTCCCTTTCTCTCATGTCAACGTGGGTACAAGGAGTCTTGGCGGGC 4788
Db 4741 CGATTTCCGGGAGTCCCTTTCTCTCATGTCAACGTGGGTACAAGGAGTCTTGGCGGGC 4800
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Db 5521 GAGGAGTATGAGGGAAGTATCTGTTCCGGCGGAGTCTCCGAGGCTCCAGGAAATTC 5580
Qy 5569 CCTCCAGCGATGCCCATATGGSCACGCCGGATTAACAACCTTCCACTGTTAGTCTGG 5628
Db 5581 CCTCCAGCGATGCCCATATGGSCACGCCGGATTAACAACCTTCCACTGTTAGTCTGG 5640
Qy 5629 AAGGACCCGAGTACGTCCTCCAGTGTGTAACCGGTGTCCATTCGCGCTGCCAGGCC 5688
Db 5641 AAGGACCCGAGTACGTCCTCCAGTGTGTAACCGGTGTCCATTCGCGCTGCCAGGCC 5700

QY	1609	GAAGAGTCAAATGGCTCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAG	1668
Db	1621	GAAGAGTCAAATGGCTCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAG	1680
QY	1669	GTACCCCAATTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG	1728
Db	1681	GTACCCCAATTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG	1740
QY	1729	TCGAGGTTAAAAACCGTCTAGGCGCCCCGAAACACGGGGAGCTGTTTCTCTTTGAAAAA	1788
Db	1741	TCGAGGTTAAAAACCGTCTAGGCGCCCCGAAACACGGGGAGCTGTTTCTCTTTGAAAAA	1800
QY	1789	CACGATAATACATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGC	1848
Db	1801	CACGATAATACATGGCGCCTATTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGC	1860
QY	1849	TGCATCATCTAGCCTCACAGGCGGGACAGGAACCAAGTTCAGGGGAGGTCCAAAGT	1908
Db	1861	TGCATCATCTAGCCTCACAGGCGGGACAGGAACCAAGTTCAGGGGAGGTCCAAAGT	1920
QY	1909	GTCTCCACCGCAACACAATCTTTCTTGGCGACCTTGCGTCAATGCGGTGCTTGCGACTGTC	1968
Db	1921	GTCTCCACCGCAACACAATCTTTCTTGGCGACCTTGCGTCAATGCGGTGCTTGCGACTGTC	1980
QY	1969	TATCATGTTGCCGCTCAAGACCCCTTGGCGGCCAAAGGGCCCCAATCAACCCAAATGTAC	2028
Db	1981	TATCATGTTGCCGCTCAAGACCCCTTGGCGGCCAAAGGGCCCCAATCAACCCAAATGTAC	2040
QY	2029	ACCAATGTGGACAGGACCTGTCGGCTGCGACAGCGCCCCCGGGGGCGGTCTCTTGACA	2088
Db	2041	ACCAATGTGGACAGGACCTGTCGGCTGCGACAGCGCCCCCGGGGGCGGTCTCTTGACA	2100
QY	2089	CCATGCACTGCGGCAGCTCGGACCTTTACTTGGTCACAGGCAATCCGATGTCATTCCG	2148
Db	2101	CCATGCACTGCGGCAGCTCGGACCTTTACTTGGTCACAGGCAATCCGATGTCATTCCG	2160
QY	2149	GTGCGCGGGGGGGCGACAGAGGGGAGCCTACTCTCCCGCAGGCCGCTCTCTACTTG	2208
Db	2161	GTGCGCGGGGGGGCGACAGAGGGGAGCCTACTCTCCCGCAGGCCGCTCTCTACTTG	2220
QY	2209	AAGGGCTCTTCGGGCGGTCCACTGCTCGCCCTCGGGGCACGTGTGGGCACTCTTCGG	2268
Db	2221	AAGGGCTCTTCGGGCGGTCCACTGCTCGCCCTCGGGGCACGTGTGGGCACTCTTCGG	2280
QY	2269	GCTGCCGTGTGCACCCGAGGGGTTGGGAAGCGCGGTGCACTTTGTACCGTCCAGTCTATG	2328
Db	2281	GCTGCCGTGTGCACCCGAGGGTTCGGAAGCGGTGCACTTTGTACCGTCCAGTCTATG	2340
QY	2329	GAACCACTATGGGTCCCGGTCTTCA CGGACAACTCGTCCCTCCGGCCGTACCGCAG	2388
Db	2341	GAACCACTATGGGTCCCGGTCTTCA CGGACAACTCGTCCCTCCGGCCGTACCGCAG	2400
QY	2389	ACATTCAGGTGCCCATCTACACGCCCTACTGGTAGCGGCAAGACACTAAGTGGCG	2448
Db	2401	ACATTCAGGTGCCCATCTACACGCCCTACTGGTAGCGGCAAGACACTAAGTGGCG	2460
QY	2449	GCTCGGTATGCAGCCCAAGGTTAAAGTGTCTTCTCTGAAACCGCTCGCGCCGCCACC	2508
Db	2461	GCTCGGTATGCAGCCCAAGGTTAAAGTGTCTTCTCTGAAACCGCTCGCGCCGCCACC	2520
QY	2509	CTAGGTTTCGGGGGTATATGTCTAAGGCACATGATCGACCCCTAACATCAGAACCGGG	2568
Db	2521	CTAGGTTTCGGGGGTATATGTCTAAGGCACATGATCGACCCCTAACATCAGAACCGGG	2580
QY	2569	GTAAAGCAATCACACGGGTGCCCATCACGTACTCCACCTATGGCAAGTTCTTGCC	2628
Db	2581	GTAAAGCAATCACACGGGTGCCCATCACGTACTCCACCTATGGCAAGTTCTTGCC	2640
QY	2629	GACGGTGGTTGCTCTCGGGGCGCCTATGACATCAATAATGTGATGAGTGCACCTCACT	2688
Db	2641	GACGGTGGTTGCTCTCGGGGCGCCTATGACATCAATAATGTGATGAGTGCACCTCACT	2700
QY	2689	GACTCGACCACTATCTGGGCACTCGGCA CAGTCTCTGGACCAAGCGGACACGGCTGGAGCG	2748

Db	2701	GACTCGACCACTATCTCTGGGCATCGGCACAGTCTCTGGACCAACGGGAGACGGCTGGAGCG	2760
QY	2749	CGACTCGTCTGCTCGCCACACCGCTACCGCTCCGGGATCGGTCAACCGTGCACATCCAAAC	2808
Db	2761	CGACTCGTCTGCTCGCCACCGCTACCGCTCCGGGATCGGTCAACCGTGCACATCCAAAC	2820
QY	2809	ATCAGGAGGTGGCTCTGTCTAGCACTGGAGAAATCCCTTTTATGCAAGACCATCCCC	2868
Db	2821	ATCAGGAGGTGGCTCTGTCTAGCACTGGAGAAATCCCTTTTATGCAAGACCATCCCC	2880
QY	2869	ATCAGAGACCATCAAGGGGGGAGACCTCATTTTCTGGCAATTCGAAGAANAATGTGAT	2928
Db	2891	ATCAGAGACCATCAAGGGGGGAGGCACTCATTTTCTGGCAATTCGAAGAANAATGTGAT	2940
QY	2929	GAGCTCGCGGAAGCTGTCTCGGCTCGGACTCAATGCTGTAGCATATTACGGGGCCCTT	2988
Db	2941	GAGCTCGCGGAAGCTGTCTCGGCTCGGACTCAATGCTGTAGCATATTACGGGGCCCTT	3000
QY	2989	GATGTATTCGTCATACCAATAGGGGAGAGCTCATTTGTCTGTAGCAACGGACGCTCTAATG	3048
Db	3001	GATGTATTCGTCATACCAATAGGGGAGAGCTCATTTGTCTGTAGCAACGGACGCTCTAATG	3060
QY	3049	ACGGGCTTTTACGGGCAATTCGACTCAGTGATCGACTGCAATACATGTCTACCCAGACA	3108
Db	3061	ACGGGCTTTTACGGGCAATTCGACTCAGTGATCGACTGCAATACATGTCTACCCAGACA	3120
QY	3109	GTCGACTTCAGCCTTGAGCCCGACCTTCACATTTAGACGACGACGCTGCCACAAGACGG	3168
Db	3121	GTCGACTTCAGCCTTGAGCCCGACCTTCACATTTAGACGACGACGCTGCCACAAGACGG	3180
QY	3169	GTGTACGCTCGACGGCGGACGAGCAGGACTGTGTAGGGCAGGATGGGCATTTACAGTTT	3228
Db	3181	GTGTACGCTCGACGGCGGACGAGCAGGACTGTGTAGGGCAGGATGGGCATTTACAGTTT	3240
QY	3229	GTGACTCCAGGAAACGGCCCTCGGCATGTCGATTTCTCGTTCTGTGCGAGTGTCTAT	3288
Db	3241	GTGACTCCAGGAAACGGCCCTCGGCATGTCGATTTCTCGTTCTGTGCGAGTGTCTAT	3300
QY	3289	GACGCGGCTGTCTGTGTACGAGCTACGCGCCGCGAGACCTCAGTTAGTTTGGGGCT	3348
Db	3301	GACGCGGCTGTCTGTGTACGAGCTACGCGCCGCGAGACCTCAGTTAGTTTGGGGCT	3360
QY	3349	TACTTAAACACACAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTCTTGGGAGAGCGTC	3408
Db	3361	TACTTAAACACACAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTCTTGGGAGAGCGTC	3420
QY	3409	TTTACAGGCTCACCCACATAGACGCCCATTTCTGTGCCAGACTAAGACGCGCAGGAGAC	3468
Db	3421	TTTACAGGCTCACCCACATAGACGCCCATTTCTGTGCCAGACTAAGACGCGCAGGAGAC	3480
QY	3469	AATCTCCCTTACTCTGTTAGCATACAGGCTACGGTGTGCGGCTCAGGCTCAGGCTCCACCT	3528
Db	3481	AATCTCCCTTACTCTGTTAGCATACAGGCTACGGTGTGCGGCTCAGGCTCAGGCTCCACCT	3540
QY	3529	CCATCTGGGACCAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCA	3588
Db	3541	CCATCTGGGACCAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCA	3600
QY	3589	ACGCCCTCTGTATAGGCTGGGACCGTTCAAAACGAGGTTATACACACACCCCATTA	3648
Db	3601	ACGCCCTCTGTATAGGCTGGGACCGTTCAAAACGAGGTTATACACACACCCCATTA	3660
QY	3649	ACCAATATCATCGCATGCTGCGCTGACCTGGAGTGTCTACGAGCACTGGGTG	3708
Db	3661	ACCAATATCATCGCATGCTGCGCTGACCTGGAGTGTCTACGAGCACTGGGTG	3720
QY	3709	CTGTAGGCGGAGTCTTAGCAGCTCTGCGCGGTATTGCTGACCAACAGGCGAGGTGTC	3768
Db	3721	CTGTAGGCGGAGTCTTAGCAGCTCTGCGCGGTATTGCTGACCAACAGGCGAGGTGTC	3780
QY	3769	ATTGTGGCGGAGTCACTTGTCTGGAAAGCCGCCATCATTTCCCGACAGGGAAGTCTTT	3828

Db	3781	ATTGTGGCAGGATCATCTTGTCCGGAAGCGGCCATCATTTCCCGCAGGGAAGTCCTT	3840
Qy	3829	TACCGGGAGTTCGATGAGATGAAGTGGCGCTCACAGCTCCCTTACATCGAAAGGGA	3888
Db	3841	TACCGGGAGTTCGATGAGATGAAGTGGCGCTCACAGCTCCCTTACATCGAAAGGGA	3900
Qy	3889	ATGCAAGTCGCGCAACATTTCAACAGAGGCAATCGGTTCTGCAACACGCCACCAAG	3948
Db	3901	ATGCAAGTCGCGCAACATTTCAACAGAGGCAATCGGTTCTGCAACACGCCACCAAG	3960
Qy	3949	CAAGCGAGGCTGCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGG	4008
Db	3961	CAAGCGAGGCTGCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGG	4020
Qy	4009	GCGAAGCATATGTGGAAATTTCAACAGGGAATCAATATTTAGCAGGCTTGTCCACTCG	4068
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Qy	4069	CTTGGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCTCTATCAACAGCCCGCTC	4128
Db	4081	CTTGGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCTCTATCAACAGCCCGCTC	4140
Qy	4129	ACCACCCAAATACCCCTCTGTTTAAATCATCTGGGGGATGGGTGGCGCGCCAACTTGCT	4188
Db	4141	ACCACCCAAATACCCCTCTGTTTAAATCATCTGGGGGATGGGTGGCGCGCCAACTTGCT	4200
Qy	4189	CTTCCAGCGCTGCTTCTGCTTTCTGATAGGCGCGGCAATCGCTGGAGGGCTGTGGCAGC	4248
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Qy	4249	ATAGGCTTGGGAAGTGTGTTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGC	4308
Db	4261	ATAGGCTTGGGAAGTGTGTTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGC	4320
Qy	4309	GCGCTCGTGCCCTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGTTAAC	4368
Db	4321	GCGCTCGTGCCCTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGTTAAC	4380
Qy	4369	CTACTCTCTGATTCCTCTCCCTGGCGCCCTAGTCTGCTGGGTGCTGCGCAGCGATA	4428
Db	4381	CTACTCTCTGATTCCTCTCCCTGGCGCCCTAGTCTGCTGGGTGCTGCGCAGCGATA	4440
Qy	4429	CTGCTCGGCACTGGGCGCAGAGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCG	4488
Db	4441	CTGCTCGGCACTGGGCGCAGAGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCG	4500
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Qy	4549	GCACTGTCACTCAGATCCTCTTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAC	4608
Db	4561	GCACTGTCACTCAGATCCTCTTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAC	4620
Qy	4609	CAGTGGATCAACGAGGACTGTCCACAGCACTGCTCCGGCTCGTGGCTAAAGAGATGTTTGG	4668
Db	4621	CAGTGGATCAACGAGGACTGTCCACAGCACTGCTCCGGCTCGTGGCTAAAGAGATGTTTGG	4680
Qy	4669	GATTGGATATGCACGGTGTGATGTGATTTAAGACTTGGCTCGAGTCCAGTCCCTGCGG	4728
Db	4681	GATTGGATATGCACGGTGTGATGTGATTTAAGACTTGGCTCGAGTCCAGTCCCTGCGG	4740
Qy	4729	CGATTGCCGGAGTCCCTCTCTTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGG	4788
Db	4741	CGATTGCCGGAGTCCCTCTCTTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGG	4800
Qy	4789	GACGCAATCATCAAAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAC	4848
Db	4801	GACGCAATCATCAAAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAC	4860
Qy	4849	GGTTCATGAGGATCGTGGGCTAGGACCTGTAGTAACAAGTGGCATGGAACTTCCCT	4908
Db	4861	GGTTCATGAGGATCGTGGGCTAGGACCTGTAGTAACAAGTGGCATGGAACTTCCCT	4920
Qy	4909	ATTAAACGGGTACACACACGGGCCCCCTTGACGCCCCCTCCCGGCGCCAAAATTATTTCTAGGGG	4968
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Qy	4969	CTGTGGCGGTGGCTGCTGAGGAGTACGTGGAGTTCAGCGGTGGGGATTTCCACTAC	5028
Db	4981	CTGTGGCGGTGGCTGCTGAGGAGTACGTGGAGTTCAGCGGTGGGGATTTCCACTAC	5040
Qy	5029	GTGACGGGCATCACCACTGACAACTGAAAGTCCCGTGTACGTTCCGCGCCCCCGAAATTC	5088
Db	5041	GTGACGGGCATCACCACTGACAACTGAAAGTCCCGTGTACGTTCCGCGCCCCCGAAATTC	5100
Qy	5089	TTTACAGAAAGTGGATGGGTGGCTGAGTACGTTTCCAGCTTCCAGCGTCCAGCGTCCCTCTTA	5148
Db	5101	TTTACAGAAAGTGGATGGGTGGCTGAGTACGTTTCCAGCTTCCAGCGTCCAGCGTCCCTCTTA	5160
Qy	5149	CGGAGGAGGTACATTTCTGGTGGGCTCAATCACTGTTTGGTTCACAGCTCCCA	5208
Db	5161	CGGAGGAGGTACATTTCTGGTGGGCTCAATCACTGTTTGGTTCACAGCTCCCA	5220
Qy	5209	TGCGAGCCGAAACCGGACGTAGCAGTGTCTTCCATGCTCACCGACCCCTCCCAATT	5268
Db	5221	TGCGAGCCGAAACCGGACGTAGCAGTGTCTTCCATGCTCACCGACCCCTCCCAATT	5280
Qy	5269	ACGGCGGAGACGGCTAAGCGTAGGTGGCCAGGGATCTCTCCCTCTCTTGGCCAGTCA	5328
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Qy	5329	TCAGTACGACGTGTCTGGCTTCTTGAAGGCAACATGCACTACCGTCTCATGCTCC	5388
Db	5341	TCAGTACGACGTGTCTGGCTTCTTGAAGGCAACATGCACTACCGTCTCATGCTCC	5400
Qy	5389	CCGAGCGCTGACCTCATCGAGGCAACCTCTCTGCGCGCAGGAGATGGCGGGAATTC	5448
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Qy	5449	ACCCGCTGGAGTCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGGAGTCTCTGG	5508
Db	5461	ACCCGCTGGAGTCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGGAGTCTCTGG	5520
Qy	5509	GAGGAGTACGAGGAGGATCGCTTCCGCGCGAGATCTGCGGAGGTCCAGGAAATTC	5568
Db	5521	GAGGAGTACGAGGAGGATCGCTTCCGCGCGAGATCTGCGGAGGTCCAGGAAATTC	5580
Qy	5569	CCTCAGCGATGCGCATATGGGCACGCGCGGATTTACAACTCCACTGTTAGAGTCTCTGG	5628
Db	5581	CCTCAGCGATGCGCATATGGGCACGCGCGGATTTACAACTCCACTGTTAGAGTCTCTGG	5640
Qy	5629	AAGGACCGGACTACGTCCCTCCAGTGGTACAGGGTGTCCATTTGCCGCTTCCAGGCGC	5688
Db	5641	AAGGACCGGACTACGTCCCTCCAGTGGTACAGGGTGTCCATTTGCCGCTTCCAGGCGC	5700
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Qy	5749	TCTGCTTTGGCGGAGCTCGCCACAAAGCCTTTCGCGAGCTCCGAATCGTGGCGGTGAC	5808
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Qy	5809	AGCGGACCGGCAACGGCTCTCTGACAGCCCTCCGAGCAGCGGAGCGCGGATCCGAC	5868
Db	5821	AGCGGACCGGCAACGGCTCTCTGACAGCCCTCCGAGCAGCGGAGCGCGGATCCGAC	5880
Qy	5869	GTTGAGTCTGCTACTCTCTCCATGCCCTTTCAGGGGAGCGCGGGGATCTCCAGTCTCAGC	5928
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Unclassified.	
REFERENCE	1 (bases 1 to 8001)
AUTHORS	Bartenschlager, R.
TITLE	Hepatitis C virus culture system
JOURNAL	Patent: US 6630343-A 16 07-OCT-2003;
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	/organism="unknown"
source	/mol_type="genomic DNA"
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Best Local Similarity 99.7%; Pred. No. 0;	
Matches 7977; Conservative 0; Mismatches 12; Indels 12; Gaps 1;	
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QY	61 TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCGAGCCCTCCAGGAC 120
DB	61 TCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCGAGCCCTCCAGGAC 120
QY	121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB	121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
QY	181 GAGCAGCGGTCCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCC 240
DB	181 GAGCAGCGGTCCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCC 240
QY	241 GCAGACTCTAGCCGAGTAGTGTGGTGCAGAAAGCCCTTGTGTACTGCTGTATAGG 300
DB	241 GCAGACTCTAGCCGAGTAGTGTGGTGCAGAAAGCCCTTGTGTACTGCTGTATAGG 300
QY	301 GTCTTCCGAGTCCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360
DB	301 GTCTTCCGAGTCCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360
QY	361 CTCAAAGAAAAACAAA-----GGGCGCGCCATGATTGAACAAGATGGATTGC 408
DB	361 CTCAAAGAAAAACAAAACGTAACCAACGCGCGCCATGATTGAACAAGATGGATTGC 420
QY	409 ACCGAGTTCTCCGCGCGCTTGGTGGAGAGGTATTCCGCTATGCTGGGCACAAAGA 468
DB	421 ACGAGGTCTTCCGCGCGCTTGGTGGAGAGGTATTCCGCTATGCTGGGCACAAAGA 480
QY	469 CAATCGGCTGCTCTGATGCCCGCGTGTTCGGCTGTGAGCGAGGGCGCCCGTTCTTT 528
DB	481 CAATCGGCTGCTCTGATGCCCGCGTGTTCGGCTGTGAGCGAGGGCGCCCGTTCTTT 540
QY	529 TTGTCAGACCGACTGTCCGGTCCCTGATGAATGAACTGCAGGACGAGCGCGGCTAT 588
DB	541 TTGTCAGACCGACTGTCCGGTCCCTGATGAATGAACTGCAGGACGAGCGCGGCTAT 600
QY	589 CGTGGTGGCCACGACGCGGTCTCTTGGCAGTGTCTGACGTTGTCTACTGAAGCGG 648
DB	601 CGTGGTGGCCACGACGCGGTCTCTTGGCAGTGTGTCTGACGTTGTCTACTGAAGCGG 660
QY	649 GAAGGGAUUGTGTCTATTGGGCGAAGTTCGGGGCAGGATCTCTGTGTCATCTCACCTTG 708
DB	661 GAAGGGAUUGTGTCTATTGGGCGAAGTTCGGGGCAGGATCTCTGTGTCATCTCACCTTG 720
QY	709 CTCCTGCCGAAAGATATCATATGCTGATGAATGCGGCGCTGCATACGCTTGATC 768
DB	721 CTCCTGCCGAAAGATATCATATGCTGATGAATGCGGCGCTGCATACGCTTGATC 780
QY	769 CGGCTACCTGCCATTCGACCAACCAAGGAAACATCGCATCGAGCGACCGTACTCGGA 828
DB	781 CGGCTACCTGCCATTCGACCAACCAAGGAAACATCGCATCGAGCGACCGTACTCGGA 840
QY	829 TGGAAAGCGGCTTGTGATATAGGATGATCTGGAGCAAGAGCATCAGGGCTCGGCCAG 888

DB	841 TGGAAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCCAG 900
QY	889 CCGAACTGTTCCAGAGGCTCAAGGCGCGCATCCCGACGCGAGGATCTCGTCGTGACCC 948
DB	901 CCGAACTGTTCCAGAGGCTCAAGGCGCGCATCCCGACGCGAGGATCTCGTCGTGACCC 960
QY	949 ATGGCGATGCTGCTTGGCGGAATATCATGTTGGAAAAATGGCGCTTTCTGGAATTCATCG 1008
DB	961 ATGGCGATGCTGCTTGGCGGAATATCATGTTGGAAAAATGGCGCTTTCTGGAATTCATCG 1020
QY	1009 ACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACATAGCTGTGGCTACCCGTGATA 1068
DB	1021 ACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACATAGCTGTGGCTACCCGTGATA 1080
QY	1069 TTGCTGAAGAGCTTGGCGCGGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCG 1128
DB	1081 TTGCTGAAGAGCTTGGCGCGGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCG 1140
QY	1129 CTCGCCATTCCGAGCGCATCGGCTTCTATCGGCTTCTTACGAGATCTTCTGAGTTTAA 1188
DB	1141 CTCGCCATTCCGAGCGCATCGGCTTCTATCGGCTTCTTACGAGATCTTCTGAGTTTAA 1200
QY	1189 CAGACCACAACGCTTTCCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1248
DB	1201 CAGACCACAACGCTTTCCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT 1260
QY	1249 AACGTTACTGGCGGAAGCGCTTGGAAATAGGCGGTGTGCGTTGTCTATATGTTATTT 1308
DB	1261 AACGTTACTGGCGGAAGCGCTTGGAAATAGGCGGTGTGCGTTGTCTATATGTTATTT 1320
QY	1309 TCACCAATATGCGGCTTCTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTG 1368
DB	1321 TCACCAATATGCGGCTTCTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTG 1380
QY	1369 ACCAGCATTCCTAGGCTCTTCCCTCTCGCCAAAGGAATCAAGTCTGTGTAATGTC 1428
DB	1381 ACCAGCATTCCTAGGCTCTTCCCTCTCGCCAAAGGAATCAAGTCTGTGTAATGTC 1440
QY	1429 GTCAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTAGGACCCCT 1488
DB	1441 GTCAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTAGGACCCCT 1500
QY	1489 TGAGGAGCGGAACCCCGCTGGGACAGGTGCTCTCGGCGCAAAAGCCACAGTGA 1548
DB	1501 TGAGGAGCGGAACCCCGCTGGGACAGGTGCTCTCGGCGCAAAAGCCACAGTGA 1560
QY	1549 TAAGATACCTGCAAGGCGGCACACCCAGTGCACCGTGTGAGTTGGATAGTTGTG 1608
DB	1561 TAAGATACCTGCAAGGCGGCACACCCAGTGCACCGTGTGAGTTGGATAGTTGTG 1620
QY	1609 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGGATGCCAGAG 1668
DB	1621 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGGATGCCAGAG 1680
QY	1669 GTACCCCATTTGATGGATCTGATCTGGGCTCTCGTGCATCTTTTACATGTTTATG 1728
DB	1681 GTACCCCATTTGATGGATCTGATCTGGGCTCTCGTGCATCTTTTACATGTTTATG 1740
QY	1729 TCAGAGTTTAAAAACGCTTAGGCCCCCGAACCAACGAGGAGCGTGGTTTCTTTGAAAA 1788
DB	1741 TCAGAGTTTAAAAACGCTTAGGCCCCCGAACCAACGAGGAGCGTGGTTTCTTTGAAAA 1800
QY	1789 CACGATTAATCAATGGGCGCTATTACGGCTTATCTCCCAACAGACGCGAGGCTTATGGC 1848
DB	1801 CACGATTAATCAATGGGCGCTATTACGGCTTATCTCCCAACAGACGCGAGGCTTATGGC 1860
QY	1849 TGCATCATCTAGCTCAGAGCGCGGACAGGAACAGAGTCCAGGGGAGGTCCAAGTG 1908
DB	1861 TGCATCATCTAGCTCAGAGCGCGGACAGGAACAGAGTCCAGGGGAGGTCCAAGTG 1920
QY	1909 GTCTCCACCGCAACACAAATCTTCTGCGGACCTCGCTCAATGGCGTGTGTTGACTGTC 1968
DB	1921 GTCTCCACCGCAACACAAATCTTCTGCGGACCTCGCTCAATGGCGTGTGTTGACTGTC 1980

QY 1969 TATCATGTGTCGGCTCAAGACCTTTGCTGCGGCCCAAGGGGCCCAATCACCCAAATGTAC 2028
DB 1981 TATCATGTGTCGGCTCAAGACCTTTGCTGCGGCCCAAGGGGCCCAATCACCCAAATGTAC 2040
QY 2029 ACCAATGTGACAGGACCTGTCGGCTGGCAAGCGCCCCCGGGGGCGGTTCTTGTGACA 2088
DB 2041 ACCAATGTGACAGGACCTGTCGGCTGGCAAGCGCCCCCGGGGGCGGTTCTTGTGACA 2100
QY 2089 CCAATGACCTGTGCGGAGCTCGGACCTTTACTTGGTCAAGAGCATGCGATGCTCATTCG 2148
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DB 2221 AAGGCTCTTTCGGGGCGTCACTGCTCTGCCCCCTCGGGGACGCTGTGGGCATCTTTTGG 2280
QY 2269 GCTGCGGTGTGACCCGAGGGGTTGCGAAGGCGGTGGACTTGTACCCGTCGAGTCTATG 2328
DB 2281 GCTGCGGTGTGACCCGAGGGGTTGCGAAGGCGGTGGACTTGTACCCGTCGAGTCTATG 2340
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DB 2341 GAAACCACTATGCGGTCTCCCGGTCTTCAAGGACAACTCGTCCCTCCGCGCGTACCGCAG 2400
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DB 2401 ACATTCAGGTGGGCCCTACTACGCCCTACTGGTACGCGCAAGTCTGTCGAGTCTATG 2460
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DB 2461 GCTGCGTATGACGCCCAAGGGTATAAGGTGTCTGCTGAACCGCTGCTGCGCGCCACC 2520
QY 2509 CTAGGTTTCGGGGGCTATATGTTAAGGACATAGGTATCGACCTTAACATCAGAACCGGG 2568
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DB 2581 GTAAGGACCATCACACCGGGTCCCTACGCTACGCTACCTTCAAGTGTCTTCTTGGC 2640
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DB 2641 GACGGTGTGCTCTGCGGGCGCTATGACATCATATATGATGATGATGATGATGATGATGAT 2700
QY 2689 GACTCGACCATATCTTGGGGATCGGCACAGTCTTGACCAAGCGGAGCGGCTGGAGCG 2748
DB 2701 GACTCGACCATATCTTGGGGATCGGCACAGTCTTGACCAAGCGGAGCGGCTGGAGCG 2760
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DB 2761 CGACTCGTGTGCTCGCCACCGCTACGCTCCGGATCGGTACCGTGCACATCCHAAAC 2820
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DB 2821 ATCGAGAGTGTGCTGTGTCAGCAGTGGAGAAATCCCTTTTATGGCAAGGCATCCCC 2880
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DB 2941 GAGTCTCGCGGAGTGTCTCGGCTCGGACTCAAGTCTGTAGCATATTAACGGGGCTT 3000
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DB 3001 GATGTATCGGTATACCAACTAGCGGAGCGTCAATTTGCTGTAGCAAGGCGCTCTAATG 3060

QY 3049 ACGGCTTTTACCGGAGTTTTCGACTCAGTGTGAGTCAATACATGTGTCAACCCAGACA 3108
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QY 3109 GTCGACTTCAGCTTGAGACCTTCCACCTTTCAGATTCAGACCGTGCACAAGACGG 3168
DB 3121 GTCGACTTCAGCTTGAGACCTTCCACCTTTCAGATTCAGACCGTGCACAAGACGG 3180
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DB 3181 GTGTTCAGCTTCAGCGCGGAGGAGGAGTCTGTAGGGGAGGATGGGATTTACAGGTTT 3240
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DB 3241 GTGACTTCAGAGAACCGGCTTCGGGATGTCGATTCCTCGGTTCTGTGAGAGTGTAT 3300
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DB 3301 GACGCGGCTGTGCTTGTGTACGAGCTCACGCCCGCGGAGACCTCAGTTAGGTTGCGGCT 3360
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DB 3361 TACTTAAACACACCGAGGTTGCCGTGTGCGAGACCACTCTGGAGTTCTGGGAGAGGCTC 3420
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QY 4069 CTTGGCAACCCCGGAGTACATCAGTGTGCAATTCACAGCTTCTATCAGCAGCGGCTC 4128
DB 4081 CTTGGCAACCCCGGAGTACATCAGTGTGCAATTCACAGCTTCTATCAGCAGCGGCTC 4140
QY 4129 ACCACCAACATACCTCTCTGTTTAACTCTTGGGGGATGGGTGGCGCCGCAACTGTCT 4188

Db	4141	ACCAACCAACATACACCTCTCTGTTTAACTCTCTGGGGGATGGGTGGCGCCCAACTTGT	4200		Db	5221	TGCGGGCCGGAACCGGACGTAGACGTGCTCACTTCCATGCTCACCGACCCCTCCACATT	5280
Qy	4189	CTTCCAGCGCTGCTTCTGCTTTTCTAGCGCGCGCATGCTGGAGCGGCTTTGGCAGC	4248		Qy	5269	ACGCGGAGACCGGCTAAGCGTAGGCTGGCCAGGGGATCTTCCCTCTCTTGGCCAGCTCA	5328
Db	4201	CTTCCAGCGCTGCTTCTGCTTTCTAGCGCGCGCATGCTGGAGCGGCTTTGGCAGC	4260		Db	5281	ACGCGGAGACCGGCTAAGCGTAGGCTGGCCAGGGATCTTCCCTCTCTTGGCCAGCTCA	5340
Qy	4249	ATAGGCTTTGGAAAGGTGCTTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGC	4308		Qy	5329	TCAGCTAGCCAGCTGCTGCGCTTCTTTGAAGGCAACATGCACTACCGTCTATGATCC	5388
Db	4261	ATAGGCTTTGGAAAGGTGCTTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGC	4320		Db	5341	TCAGCTAGCCAGCTGCTGCGCTTCTTTGAAGGCAACATGCACTACCGTCTATGATCC	5400
Qy	4309	GGCTGCTGGCTTTAAGGTCATAGCGCGAGATGCCCTCCACAGGACCTGTTTAAAC	4368		Qy	5389	CGGACGCTGACCTCATCGAGGCGAACCTCTGTCGCGCAGAGATGGCGGGAAACATC	5448
Db	4321	GGCTGCTGGCTTTAAGGTCATAGCGCGAGATGCCCTCCACAGGACCTGTTTAAAC	4380		Db	5401	CGGACGCTGACCTCATCGAGGCGAACCTCTCTGTCGCGCAGAGATGGCGGGAAACATC	5460
Qy	4369	CTACTCCCTGCTATCTCTCCCTTGGCGCCCTAGTCTGCTGGGTGCTGTCGCGAGGATA	4428		Qy	5449	ACCGCGTGGAGTACAGAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5508
Db	4381	CTACTCCCTGCTATCTCTCTCCCTTGGCGCCCTAGTCTGCTGGGTGCTGTCGCGAGGATA	4440		Db	5461	ACCGCGTGGAGTACAGAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5520
Qy	4429	CTGGTGGGACGCTGGGCGCCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGATAGCG	4488		Qy	5509	GAGGAGATGAGAGGGAAGTATCCGTTCCGGGGAGATCTTGGGAGGTCCAGGAAATTC	5568
Db	4441	CTGGTGGGACGCTGGGCGCCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGATAGCG	4500		Db	5521	GAGGAGATGAGAGGGAAGTATCCGTTCCGGGGAGATCTTGGGAGGTCCAGGAAATTC	5580
Qy	4489	TTGCTTTGCGGGGTAAACACGCTCTCCCGCACGCACTATGTGCTGAGAGCGACGCTGCA	4548		Qy	5569	CCTCGAGCGATGCCATATGGGACGCGCGGATTACAACCTCCACTGTTTAGAGTCTGTG	5628
Db	4501	TTGCTTTGCGGGGTAAACACGCTCTCCCGCACGCACTATGTGCTGAGAGCGACGCTGCA	4560		Db	5581	CCTCGAGCGATGCCATATGGGACGCGCGGATTACAACCTCCACTGTTTAGAGTCTGTG	5640
Qy	4549	GCAGTGTCACTCAGATCTCTTAGTCTTACATCACTCAGCTGTGTAAGAGGCTTCAC	4608		Qy	5629	AAGGACCCGAGCTACCTCCCTCCAGTGGTACACGGGTGTCATGTCGCGCTGCCAAGGCC	5688
Db	4561	GCAGTGTCACTCAGATCTCTTAGTCTTACCATCACTCAGCTGTGTAAGAGGCTTCAC	4620		Db	5641	AAGGACCCGAGCTACCTCCCTCCAGTGGTACACGGGTGTCATGTCGCGCTGCCAAGGCC	5700
Qy	4609	CAGTGTCAACAGGACTGCTCCAGCCATGCTCCGGCTGCTGGCTTAAGAGATGTTGG	4668		Qy	5689	CCTCCGATACCTCCAAGGAGAGAGGACGGTGTCTGTCGCAAGATCTACCGTGTCT	5748
Db	4621	CAGTGTCAACAGGACTGCTCCAGCCATGCTCCGGCTGCTGGCTTAAGAGATGTTGG	4680		Db	5701	CCTCCGATACCTCCAAGGAGAGAGGACGGTGTCTGTCGCAAGATCTACCGTGTCT	5760
Qy	4669	GATTGGATACGACGGTGTGACTGATTCAAGACCTGGCTCCAGTCCCAAGCTCTGCGG	4728		Qy	5749	TCCTGCTTGGCGAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCTCGAC	5808
Db	4681	GATTGGATACGACGGTGTGACTGATTCAAGACCTGGCTCCAGTCCCAAGCTCTGCGG	4740		Db	5761	TCCTGCTTGGCGAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCTCGAC	5820
Qy	4729	CGATTGCGGGAGTCCCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGC	4788		Qy	5809	AGCGGACCGCAACGGCTCTCTGACAGCCCTTCGACGACGCGCGAGCGGGATCCGAC	5868
Db	4741	CGATTGCGGGAGTCCCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGC	4800		Db	5821	AGCGGACCGCAACGGCTCTCTGACAGCCCTTCGACGACGCGCGAGCGGGATCCGAC	5880
Qy	4789	GACGGCATATGCAAAACCACTGCGCATGTGGAGCAGACATCACCGACATGTCAAAAAC	4848		Qy	5869	GTTGAGTGTACTCTTCTCATGTGCGGGGAGCGGGGATCCGATCTCAGC	5928
Db	4801	GACGGCATATGCAAAACCACTGCGCATGTGGAGCAGACATCACCGACATGTGAAAAC	4860		Db	5881	GTTGAGTGTACTCTTCTCATGTGCGGGGAGCGGGGATCCGATCTCAGC	5940
Qy	4849	GTTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCC	4908		Qy	5929	GACGGCTTTGGTCTACCGTAAAGCGAGGAGCTAGTACAGACGCTGCTGCTCGATG	5988
Db	4861	GTTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCC	4920		Db	5941	GACGGCTTTGGTCTACCGTAAAGCGAGGAGCTAGTACAGACGCTGCTGCTCGATG	6000
Qy	4909	ATTAAACGGTACACACGGGCGCTTGACAGCCCTCCCGGGCGCAAAATTTCTAGGGCG	4968		Qy	5989	TCCTACACATGGAAGCGGCGCTGATCAAGCCTGCGTGGGAGGAAACCAAGCTGCC	6048
Db	4921	ATTAAACGGTACACACGGGCGCTTGACAGCCCTCCCGGGCGCAAAATTTCTAGGGCG	4980		Db	6001	TCCTACACATGGAAGCGGCGCTGATCAAGCCTGCGTGGGAGGAAACCAAGCTGCC	6060
Qy	4969	CTGTGGGGTGGCTGCTGAGGATGAGTGGAGGTTACGCGGGTGGGGAATTTCCACTAC	5028		Qy	6049	ATCAATGCACTGACCACTCTTTGCTCGGTCAACACACTTGGTCTAGCTACACATCT	6108
Db	4981	CTGTGGGGTGGCTGCTGAGGATGAGTGGAGGTTACGCGGGTGGGGAATTTCCACTAC	5040		Db	6061	GTCATGCACTGAGCAACTCTTTCTCGTCCGTCACCAACTTGGTCTAGCTACACATCT	6120
Qy	5029	GTGACGGGATGACCACTGACAAAGTAAAGTGCCTGCTGAGGTTCCGGGCCCCGGAATTC	5088		Qy	6109	CGCAGCGCAAGCTTGGCGGAGAGGTCACTTTTGACAGACTGCGGTCCTGCGACGAC	6168
Db	5041	GTGACGGGATGACCACTGACAAAGTAAAGTGCCTGCTGAGGTTCCGGGCCCCGGAATTC	5100		Db	6121	CGCAGCGCAAGCTTGGCGGAGAGAGGTCACTTTTGACAGACTGCGGTCCTGCGACGAC	6180
Qy	5089	TTCCAGAGTGGATGGGGTGGGTGACAGGTACGCTCCAGCGTCAAAACCCCTCCTA	5148		Qy	6169	CACCTACCGGAGCTGCTCAAGGAGATGAAGCGGAAGCGGTCCAAGTTAAGGCTAACTT	6228
Db	5101	TTCCAGAGTGGATGGGGTGGGTGACAGGTACGCTCCAGCGTCAAAACCCCTCCTA	5160		Db	6181	CACCTACCGGAGCTGCTCAAGGAGATGAAGCGGAAGCGGTCCAAGTTAAGGCTAACTT	6240
Qy	5149	CGGAGGAGGTACATCTCTGCTCGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA	5208		Qy	6229	CTATCCGTTGGAGGAGCTTAAAGTCAAGCGCCCGACACTTCGCGCAGATCTAAATTTGCG	6288
Db	5161	CGGAGGAGGTACATCTCTGCTCGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA	5220		Db	6241	CTATCCGTTGGAGGAGCTTAAAGTCAAGCGCCCGACACTTCGCGCAGATCTAAATTTGCG	6300
Qy	5209	TGCGAGCCCGGAACCGGACGTAGAGTGTCACTTCAATGCTCAACGACCCCTCCACATT	5268		Qy	6289	TATGGGCAAGGAGCTCCGGAACCTATCCAGCAGGCGGCTTAAACCACTCCGCTCCGTG	6348
					Db	6301	TATGGGCAAGGAGCTCCGGAACCTATCCAGCAGGCGGCTTAAACCACTCCGCTCCGTG	6360

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DEFINITION Sequence 6 from Patent EP1043399.
ACCESSION AX036257
VERSION AX036257.1 GI:11225873
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Bartschlagher R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
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ORIGIN

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AUTHORS Bartenschlager,R.
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Db 4261 ATAGGCTCTGGGAGGCTGTGGATATTTTGGCAGGTTATGGAGCGGCTGGCAGGC 4320
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QY	5449	ACCGCGTGGAGTCA	GAATAAGGTAGT	ATATTTGG	ACTCTTT	CGAGCCGCTCCA	AGCG	5508	
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QY	5509	GAGGAGGATGAGAG	GGAAGTATCC	CGTCCG	CGGAGATCT	CTCGGAGT	TCAGGAAATTC	5568	
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QY	5569	CCTCGAGCGATGCC	ATATGGGCA	CGCCCGGATTA	CAACCCCTC	CACTGTTAG	AGTCTCTG	5628	
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RESULT 13
AX036261

LOCUS AX036261 8001 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 10 from Patent EP1043399.
ACCESSION AX036261
VERSION AX036261.1 GI:11225877
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1
AUTHORS Bartenschlager, R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 10 11-OCR-2000;
BARTENSCHLAGER RALF DR (DE)
FEATURES
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Query Match 99.4%; Score 7941.4; DB 6; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

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Db	3121	GTGCACTTCAGGCTCGGACCCGACCTTCACCATTCAGACGACGCGTCCACAAAGACGG	3180
Qy	3169	GTGTCACGCTCGACGGCGAGGACGAGTCTGTAAGGGGACGATGGGCATTTACAGGTTT	3228
Db	3181	GTGTCACGCTCGACGGCGAGGAGTCTGTAAGGGGACGATGGGCATTTACAGGTTT	3240
Qy	3229	GTGACTTCCAGGAGAACGGCCCTCGGGCATGTTCGATTTCTCGGTTCTGTGCGAGTGCTAT	3288
Db	3241	GTGACTTCCAGGAGAACGGCCCTCGGGCATGTTCGATTTCTCGGTTCTGTGCGAGTGCTAT	3300
Qy	3289	GACGGGGCTGTGTTGTGTAGCAGCTCAACGCCGCCGAGACCTCAGTTAGTTGGGGCT	3348
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Qy	3349	TACCTAAACACACAGGTTGCCGTCTGCAGGACCATCTGGAGTTCTGGGAGACGCTC	3408
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Qy	3409	TTTACAGSCCTCACCCATAGACGCCCATTTCTTTGCCAGACTAAGCAGGACGAGAC	3468
Db	3421	TTTACAGSCCTCACCCATAGACGCCCATTTCTTTGCCAGACTAAGCAGGACGAGAC	3480
Qy	3469	AACTTCCCTACCTGGTAGCATACGAGCTACGGTGTGCGCAGGACTCAGGCTCCACT	3528
Db	3481	AACTTCCCTACCTGGTAGCATACGAGCTACGGTGTGCGCAGGACTCAGGCTCCACT	3540
Qy	3529	CCATCTGGGACCAAATGTGGAAAGTCTCATACGGCTAAAGCTACGCTGCACGGGCA	3588
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Qy	3709	CTGGTAGGCGAGTCTAGCAGCTCTTGGCGGGTATTTGCTTCAACACAGGACGCTGTC	3768
Db	3721	CTGGTAGGCGAGTCTAGCAGCTCTTGGCGGGTATTTGCTTCAACACAGGACGCTGTC	3780
Qy	3769	ATTGTGGGACGAGTCACTTTGTCGGAAGACGGCCATCATTTCCCGACAGGAAAGTCCTT	3828
Db	3781	ATTGTGGGACGAGTCACTTTGTCGGAAGACGGCCATCATTTCCCGACAGGAAAGTCCTT	3840
Qy	3829	TACGGGAGTTGATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAACGGA	3888
Db	3841	TACGGGAGTTGATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAACGGA	3900
Qy	3889	ATCAGCTCGCGAAACAATTCAAACAGAGGCAATCGGGTTCTGSCAAACAGCCACCAAG	3948
Db	3901	ATCAGCTCGCGCGAAACAATTCAAACAGAGGCAATCGGGTTCTGSCAAACAGCCACCAAG	3960
Qy	3949	CAAGCGGAGCTCTGCTCCCTGCTGGTGGATCCAAAGTGGCGGACCTCGAAGCCTCTGG	4008
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Qy	4069	CTGGGCAACCCCGCGGATAGCATCACTGATGGCAATTCACAGCCTCTATCACCAGCCCGCTC	4128
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Qy	4189	CTTCCAGCGCTGTCTCTCTTTCGTAGCGCCCGGCATCGCTGAGCGGCTGTGGCAGC	4248
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Db	4921	ATTAAACGGTACCAACGCGGCCCTTGCAAGCTCCCGCGGCCAAATTTATCTAGGGCG	4980
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ACCESSION AX937622
VERSION AX937622.1 GI:40713673
KEYWORDS
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1
AUTHORS Duggal, R.A., Patrick, A.K., Zhang, J.A. and Zhao, W.A.
TITLE Reporter-selectable hepatitis c virus replicon
JOURNAL Patent: WO 03091439-A 2 06-NOV-2003;
PRIZER INC. (US)
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ORIGIN

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QY	1578	CCAGTGCACGTTGTGAGTGGATGTTGTGGAAGAGTCAATGCTCTCTCTCAAGCGT	1637	QY	2658	CATCATATATGTGATGAGTGCACATCAACTGACTGACCACTATCTCTGGGCATCGGCAC	2717
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QY	1638	ATTCAACAGGGGCTCAAGATGCCAGAAAGTACCCCAATTGATGGGATCTGATCGG	1697	QY	2718	AGTCTCTGGAACGAGACGCGTGGAGCGGACTCGTCTGCTCGCCACCGCTACGCC	2777
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QY	1698	GCCTCGGTGCACATGCTTTACATGTTTGTAGTGCAGGTTAAAAAGTCTAGGCCGCCCG	1757	QY	2778	TCCGGGATCGGTCAACGTCGCCACATCCAAACATCGAGGAGGTGGCTCTGTCACGACTGG	2837
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QY	1758	AACACGGGGACGTGTTTCTTTGAAAACAGGATAATACCATGGCGCTATTACGGC	1817	QY	2838	AGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGGAGGACCT	2897
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QY	1818	CTACTCCCAACAGACGCGGCTTACTTGGCTGCATCATCACTAGCCTCAAGGCCCGGA	1877	QY	2898	CATTTCTGCTCATTCAGAAAGAAATGTGATGAGCTCGCCGCGAAAGCTGTCGCGCTCGG	2957
Db	2810	CTACTCCCAACAGACGCGGCTTACTTGGCTGCATCATCACTAGCCTCAAGGCCCGGA	2869	Db	3890	CATTTCTGCTCATTCAGAAAGAAATGTGATGAGCTCGCCGCGAAAGCTGTCGCGCTCGG	3949
QY	1878	CAGGAACACAGTCCAGGGGAGGTCCAAAGTGTCTCAACCGCAACAATCTTCTTGGC	1937	QY	2958	ACTCAATGCTGTAGCATATTACCGGGCTTTGATGATTCGCTCATACCAACTAGCGAGA	3017
Db	2870	CAGGAACACAGTCCAGGGGAGGTCCAAAGTGTCTCAACCGCAACAATCTTCTTGGC	2929	Db	3950	ACTCAATGCTGTAGCATATTACCGGGCTTTGATGATTCGCTCATACCAACTAGCGAGA	4009
QY	1938	GACCTGGTCAATGGCGTGTGTTGACTGTTATGTTGCTGCTGCTCAAGAGACCTTGC	1997	QY	3018	CGTCAATGCTGTAGCAAGACGCTCTAATGAGCGGCTTTACCGGCGATTTTCGACTCAGT	3077
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QY	1998	CGGCCCAAGGGCCCAATCACCAAAATGTACCAAAATGTGACACGAGACCTCTCGGCTG	2057	QY	3078	GATCGCTGCAATACATGTTGTACCCAGACAGTCCAGCTTCAGGCTGGACCCGACTTCAC	3137
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Db	3050	GCAAGCGCCCGCCGGGGCGGTTCTTGAACACCATGACACCATGACCTGCGGACCTTTA	3109	Db	4130	CATTGAGACGACGACCGGTGCCAAGACGCGGTGTACGCTTCGACGCGCGGCGAGGAC	4189
QY	2118	CTTGGTCAAGGATGCGGATGTCATTCGCGTGGCGGCGGCGGCGAGCAGCGGGGAG	2177	QY	3198	TGGTAGGGGACGAGTGGGCAATTTACAGGTTTGTGACTCCAGGAGAACGGCCCTCGGGCAT	3257
Db	3110	CTTGGTCAAGGATGCGGATGTCATTCGCGTGGCGGCGGCGGCGAGCAGCGGGGAG	3169	Db	4190	TGGTAGGGGACGAGTGGGCAATTTACAGGTTTGTGACTCCAGGAGAACGGCCCTCGGGCAT	4249
QY	2178	CCTACTCTCCCGCCAGGCGGCTCTCTACTTGAAGGGCTCTTGGGGGGTCCACTGCTCTG	2237	QY	3258	GTTTCGATTCCTCGGTTCTGTCGAGTGTATGACGCGGGCTGTGCTTGGTACGAGCTCAC	3317
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QY	2358	GGCAACTCGTCCCTCCCGCGGTACCGCAGACATTCAGGTGGGCCCATCTACGCCCC	2417	QY	3438	TTTCTTGTCCCAAGACTAAGCAGGACGAGACAACTTCCCTTACCTGGTAGCATACAGGC	3497
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[illegible]

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VERSION AX937621.1 GI:40713672
KEYWORDS
SOURCE unidentifed
ORGANISM unidentifed
unclassified.
1
REFERENCE
AUTHORS Duggal,R.A., Patrick,A.K., Zhang,J.A. and Zhao,W.A.
TITLE Reporter-selectable hepatitis c virus replicon
JOURNAL Patent: WO 03091439-A 1 06-NOV-2003;
PFIZER INC. (US)
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Qy 1698 GCCTCGGTGCACATGCTTTACATGTTTGTAGTGAAGGTAAACACGCTAGGCGCGCGC 1757
Db 2860 GCCTCGGTGCACATGCTTTACATGTTTGTAGTGAAGGTAAACACGCTAGGCGCGCGC 2919
Qy 1758 AACACCGGGAGCTGTTTCTTTGAAACACGATTAATACCATGCGGCTATTACGGC 1817
Db 2920 AACACCGGGAGCTGTTTCTTTGAAACACGATTAATACCATGCGGCTATTACGGC 2979
Qy 1818 CTACTCCACACGCGGCGCTACTTGTGCTGATCATCATAGCTCAAGCGCGGA 1877
Db 2980 CTACTCCACACGCGGCGCTACTTGTGCTGATCATCATAGCTCAAGCGCGGA 3039
Qy 1878 CAGGAACCAAGGTGCGGGGAGGTCAAAGTGTCTCCACCGCAACACATCTTCTTCCG 1937
Db 3040 CAGGAACCAAGGTGCGGGGAGGTCAAAGTGTCTCCACCGCAACACATCTTCTTCCG 3099
Qy 1938 GACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGCGCTCAAGACCTTGC 1997
Db 3100 GACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGCGCTCAAGACCTTGC 3159
Qy 1998 CGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGACCAAGACTCTGTCGCGTG 2057
Db 3160 CGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGACCAAGACTCTGTCGCGTG 3219
Qy 2058 GCAAGCGCGCGCGCGGCTTCTTGTGACCATGACCTGCGGCGAGCTCGGACCTTTA 2117
|||||

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Qy 2118 CTTTGGTCAAGAGCATGCGATGTCTCATTCGGTGGCCCGGCGGGGCGACAGAGGGGGAG 2177
Db 3280 CTTTGGTCAAGAGCATGCGATGTCTCATTCGGTGGCCCGGCGGGGCGACAGAGGGGGAG 3339
Qy 2178 CTTTGGTCAAGAGCATGCGATGTCTCATTCGGTGGCCCGGCGGGGCGACAGAGGGGGAG 2237
Db 3340 CTTTGGTCAAGAGCATGCGATGTCTCATTCGGTGGCCCGGCGGGGCGACAGAGGGGGAG 3399
Qy 2238 CCGCTCGGGGCAAGCTGTGGGATCTTTTCGGGCTGCGGTGTCACCGCGAGGGTTCGAA 2297
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Qy 2298 GCGGTGGACTTTGTACCGGTGAGTCTATPAAAAACAATATGCGGTGCCCGTCTTCAC 2357
Db 3460 GCGGTGGACTTTGTACCGGTGAGTCTATPAAAAACAATATGCGGTGCCCGTCTTCAC 3519
Qy 2358 GGAACAATCGTCCCTCGGCGGTACCGGAGACATTCAGGTGGCCCATCTACACGCCCC 2417
Db 3520 GGAACAATCGTCCCTCGGCGGTACCGGAGACATTCAGGTGGCCCATCTACACGCCCC 3579
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Db 3580 TACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGACAGCCCAAGGGTATAAGT 3639
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Db 4240 GATGACTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4299
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Db 4300 CATTTGAGAGGACCGGTGCAACAGACGGGTGTCAAGCGGGTGTCAAGCGGGGAGGAGAC 4359

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QY 4578 TACCATCACTGCTGCTGAAGGGTTTCAAGAGGTTTCAAGAGGAGTCAACAGGAGTCTTCCACGCC 4637
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Db 5980 TGGACACAGATCACCGGACATGTCAAAACCGTTTCCATGAGGATCGTGGGCGCTTAGGAC 6039
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Search completed: November 2, 2004, 01:52:47
Job time : 21431 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 17:15:25 ; Search time 398 Seconds
(without alignments)
14272.926 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7967	99.7	8001	4	US-09-539-601-7
3	7949.4	99.5	8001	4	US-09-539-601-22
4	7947.8	99.4	8001	4	US-09-539-601-16
5	7941.4	99.4	8001	4	US-09-539-601-28
6	7331	91.7	8637	4	US-09-539-601-4
7	7309	91.5	8649	4	US-09-539-601-13
8	7273.8	91.0	8639	4	US-10-029-907-1
9	7272.8	91.0	8638	4	US-10-029-907-24
10	7249.8	90.7	8638	4	US-10-029-907-7
11	7248.8	90.7	8638	4	US-10-029-907-25
12	7246.8	90.7	8642	4	US-10-029-907-2
13	7245.6	90.7	8638	4	US-10-029-907-6
14	7229.8	90.5	8648	4	US-10-029-907-5
15	7222.6	90.4	8643	4	US-10-029-907-4
16	6186.8	77.4	11076	4	US-09-539-601-1
17	6169.2	77.2	11076	4	US-09-539-601-25
18	6167.6	77.2	11076	4	US-09-539-601-19
19	6161.2	77.1	11076	4	US-09-539-601-31
20	5318.4	66.5	9595	3	US-09-014-416-4
21	5218	65.3	7917	1	US-08-324-977-31
22	5218	65.3	7917	2	US-08-384-616-31
23	5218	65.3	7917	3	US-08-904-686A-31
24	5218	65.3	7917	3	US-09-315-850-31
25	5218	65.3	9416	1	US-08-324-977-1
26	5218	65.3	9416	2	US-08-384-616-1
27	5218	65.3	9416	2	US-08-904-686A-1

28 5218 65.3 9416 3 US-09-315-850-1 Sequence 1, Appli
29 5218 65.3 9416 4 US-08-823-895A-27 Sequence 27, Appli
30 5211.8 65.2 9472 1 US-08-150-204E-96 Sequence 96, Appli
31 5175.2 64.8 7863 1 US-08-324-977-35 Sequence 35, Appli
32 5175.2 64.8 7863 2 US-08-384-616-35 Sequence 35, Appli
33 5175.2 64.8 7863 2 US-08-904-686A-35 Sequence 35, Appli
34 5175.2 64.8 7863 3 US-08-315-850-35 Sequence 35, Appli
35 5175.2 64.8 9030 1 US-08-324-977-13 Sequence 13, Appli
36 5175.2 64.8 9030 2 US-08-384-616-13 Sequence 13, Appli
37 5175.2 64.8 9030 3 US-08-904-686A-13 Sequence 13, Appli
38 5175.2 64.8 9030 3 US-09-315-850-13 Sequence 13, Appli
39 4103.8 51.3 9599 3 US-09-014-416-2 Sequence 2, Appli
40 4102.2 51.3 9599 3 US-09-014-416-6 Sequence 2, Appli
41 4097.8 51.3 9646 3 US-08-811-566-1 Sequence 1, Appli
42 4097.8 51.3 9646 3 US-09-034-756-1 Sequence 1, Appli
43 4094.2 51.2 12980 3 US-08-811-566-5 Sequence 5, Appli
44 4094.2 51.2 12980 3 US-09-034-756-5 Sequence 5, Appli
45 4021.4 50.3 9379 3 US-09-388-874-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-539-601-10
; Sequence 10, Application US/09539601C
; Patent No. 8630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1801)..(7758)
; OTHER INFORMATION: hepatitis C virus NS3 - 5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7759)..(7989)
; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
; AUTHORS: Krner, Frank
; AUTHORS: Koch, Jan-Oliver
; AUTHORS: Herian, Ulrike
; AUTHORS: Theilmann, Lorenz
; AUTHORS: Bartenschlager, Ralf
; TITLE: Replication of subgenomic hepatitis C virus RNAs in a
; JOURNAL: Science
; VOLUME: 285

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DATE: 1999-07-02									
US-09-539-601-10									
Query Match 100.0%; Score 7989; DB 4; Length 7989;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	1	GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60						
QY	61	TCTTCAACGAGAAACGCTAGCCATAGCCATAGCGGTAGTATGAGTGTCTGAGCTCCAGAC	120						
Db	61	TCTTCAACGAGAAACGCTAGCCATAGCCATAGCGGTAGTATGAGTGTCTGAGCTCCAGAC	120						
QY	121	CCCCCTCCCGGAGAGCATAGTGTCTGCGAAACCGGTAGTACACCGGAATGGCCAG	180						
Db	121	CCCCCTCCCGGAGAGCATAGTGTCTGCGAAACCGGTAGTACACCGGAATGGCCAG	180						
QY	181	GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGCTGCCGCC	240						
Db	181	GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGCTGCCGCC	240						
QY	241	GGGAGCTCTAGCCGAGTGTGTTGGGTGCGAAGGCTTGTGTACTGCTGATAGG	300						
Db	241	GGGAGCTCTAGCCGAGTGTGTTGGGTGCGAAGGCTTGTGTACTGCTGATAGG	300						
QY	301	GTGCTTGGAGTGTCCCGGAGGTCTGCTAGACCGGTGACCATGAGCAAGATCCTAAAC	360						
Db	301	GTGCTTGGAGTGTCCCGGAGGTCTGCTAGACCGGTGACCATGAGCAAGATCCTAAAC	360						
QY	361	CTCAAGAAAAACAAAGGCGCGCATGATGAAACAAGATGATGCGAGGATTTCTC	420						
Db	361	CTCAAGAAAAACAAAGGCGCGCATGATGAAACAAGATGATGCGAGGATTTCTC	420						
QY	421	CGGCCGCTTGGGTGGAGAGCTATTGGGTATGACTGGGCACACAGACATCGGTGCT	480						
Db	421	CGGCCGCTTGGGTGGAGAGCTATTGGGTATGACTGGGCACACAGACATCGGTGCT	480						
QY	481	CTGATGCGCGGTGTTCCGGCTGTACGCGAGGGGCGCGGTCTTTTGTCAAGACCG	540						
Db	481	CTGATGCGCGGTGTTCCGGCTGTACGCGAGGGGCGCGGTCTTTTGTCAAGACCG	540						
QY	541	ACCTGTCCGGTGGCTGAATGAATGACGAGGAGCGCGGTATCTGTGCTGCCA	600						
Db	541	ACCTGTCCGGTGGCTGAATGAATGACGAGGAGCGCGGTATCTGTGCTGCCA	600						
QY	601	CGAGCGGCTTCTTGGCGAGCTGTGCTGACGCTTGTCACTGAAGCGGAAGGACTGGC	660						
Db	601	CGAGCGGCTTCTTGGCGAGCTGTGCTGACGCTTGTCACTGAAGCGGAAGGACTGGC	660						
QY	661	TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCTTGTGCCAGA	720						
Db	661	TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCTTGTGCCAGA	720						
QY	721	AAGTATCCATCATGGCTGATGAATGCGCGGTGCTATGCTGTGATCGGGCTACCTGCC	780						
Db	721	AAGTATCCATCATGGCTGATGAATGCGCGGTGCTATGCTGTGATCGGGCTACCTGCC	780						
QY	781	CATTGACCAACAGCGAATCATCGATCGAGCGAGCAGTCTCGATGGAAGCGGCTC	840						
Db	781	CATTGACCAACAGCGAATCATCGATCGAGCGAGCAGTCTCGATGGAAGCGGCTC	840						
QY	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCCAGCCGAACTGTCG	900						
Db	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCCAGCCGAACTGTCG	900						
QY	901	CCAGGCTCAAGCGCGGATGCTCCGAGCGGAGGATCTGCTGACCATGCGCATGCT	960						
Db	901	CCAGGCTCAAGCGCGGATGCTCCGAGCGGAGGATCTGCTGACCATGCGCATGCT	960						
QY	961	GCTTCCGAAATCATGTGGTGGAAATGGCCGCTTTTCTGGATTATCGACTGTGCGCGG	1020						

Db	2041	CAGGACCTCGTCGGCTGCGAAGCGCCCGCCGGGGCGGCTTCCTTGACACCATGCACTGC	2100
Qy	2101	GGCAGCTCGGACTTTTACTTTGGTTCACAGGCGCATGCCGATGTCATTCGGTGCGCCGGCGG	2160
Db	2101	GGCAGCTCGGACCTTTACTTTGGTTCACAGGCGCATGCCGATGTCATTCGGTGCGCCGGCGG	2160
Qy	2161	GGCGACAGAGGGGAGCGTACTCTCCCCAGGCGCGTCTCCTACTTGAAGGCTCTTCG	2220
Db	2161	GGCGACAGAGGGGAGCGTACTCTCCCCAGGCGCGTCTCCTACTTGAAGGCTCTTCG	2220
Qy	2221	GGCGCTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATCTTCGGGCTCCGCTGTCG	2280
Db	2221	GGCGCTCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCATCTTCGGGCTCCGCTGTCG	2280
Qy	2281	ACCGAGGGGTGGGAAGCGCGTGACCTTTGPAACCGCTCGAGCTCATGGAACACCACTATG	2340
Db	2281	ACCGAGGGGTGGGAAGCGCGTGACCTTTGPAACCGCTCGAGCTCATGGAACACCACTATG	2340
Qy	2341	CGGTCCCGGTCTTTCACGGAACAATCGTCCCTCCGGCCGTACCGACAGACATTCCAGGTG	2400
Db	2341	CGGTCCCGGTCTTTCACGGAACAATCGTCCCTCCGGCCGTACCGACAGACATTCCAGGTG	2400
Qy	2401	GCCCATCTACACGCCCTTACTGTTAGCGGCAAGAGCACTAAGTGCCTGGCTGCGTATGCA	2460
Db	2401	GCCCATCTACACGCCCTTACTGTTAGCGGCAAGAGCACTAAGTGCCTGGCTGCGTATGCA	2460
Qy	2461	GCCCAAGGGTATAGGTCCTTGCTGCTGAACCCGTCGGTCGCGCCACCTAGGTTTCGGG	2520
Db	2461	GCCCAAGGGTATAGGTCCTTGCTGCTGAACCCGTCGGTCGCGCCACCTAGGTTTCGGG	2520
Qy	2521	GCCTATATGCTTAAGGCACATGGTATGCACTTAACATCAGAACCGGGGTAAAGCACTC	2580
Db	2521	GCCTATATGCTTAAGGCACATGGTATGCACTTAACATCAGAACCGGGGTAAAGCACTC	2580
Qy	2581	ACCACGGGTCCCCCATCAAGTACTCCACCTATGCGCAAGTTTCTTGCAGCGGTGGTTGC	2640
Db	2581	ACCACGGGTCCCCCATCAAGTACTCCACCTATGCGCAAGTTTCTTGCAGCGGTGGTTGC	2640
Qy	2641	TCGTGGGGCGCTATGACATCAATAATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700
Db	2641	TCGTGGGGCGCTATGACATCAATAATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700
Qy	2701	ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG	2760
Qy	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACCATCAAAATCGAGGAGGTG	2820
Db	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACCATCAAAATCGAGGAGGTG	2820
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGAAAGCCATCCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGAAAGCCATCCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGACCTCAATTTCTGGCATTCGAAGAAATGTGATGAGCTCGCGCG	2940
Db	2881	AAGGGGGGAGGACCTCAATTTCTGGCATTCGAAGAAATGTGATGAGCTCGCGCG	2940
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACGGGGCCCTTGATGATCCGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACGGGGCCCTTGATGATCCGTC	3000
Qy	3001	ATACCAACTAGCGGAGAGTCAATTGTCGTAGCAACGGAGCGCTCAATGACGGCTTTACC	3060
Db	3001	ATACCAACTAGCGGAGAGTCAATTGTCGTAGCAACGGAGCGCTCAATGACGGCTTTACC	3060
Qy	3061	GGCGATTTGCACTGATGATCGACTGCAATCATGTGTCAACCGACAGTGCAGCTTCAG	3120
Db	3061	GGCGATTTGCACTGATGATCGACTGCAATCATGTGTCAACCGACAGTGCAGCTTCAG	3120
Qy	3121	CTGGACCCGCACTTCACCATTGAGACGACGACCTGTCACACAGACGGGTGTCAGCTCG	3180
Db	3121	CTGGACCCGCACTTCACCATTGAGACGACGACCTGTCACACAGACGGGTGTCAGCTCG	3180

QY	3181	CAGCGGCGAGCAGGACTGGTAGGGCGCAGGATGGGCATTTACAGGTTTGTGTGACTCCAGGA	3240
DB	3181	CAGCGGCGAGCAGGACTGGTAGGGCGCAGGATGGGCATTTACAGGTTTGTGTGACTCCAGGA	3240
QY	3241	GAAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACCGGGGCTGT	3300
DB	3241	GAAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACCGGGGCTGT	3300
QY	3301	GCTTGGTACGAGCTCAGCCCGCCGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACACA	3360
DB	3301	GCTTGGTACGAGCTCAGCCCGCCGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACACA	3360
QY	3361	CCAGGGTGCOCGTCCTCCAGGACCATCTGGAGTTCTGGGAGAGGCTCTTTACAGGCCTC	3420
DB	3361	CCAGGGTGCOCGTCCTCCAGGACCATCTGGAGTTCTGGGAGAGGCTCTTTACAGGCCTC	3420
QY	3421	ACCCACATAGACGCCCATTTCTTGTCCGAGACTAAGCAGGCGAGGAGACAACCTTCCCTTAC	3480
DB	3421	ACCCACATAGACGCCCATTTCTTGTCCGAGACTAAGCAGGCGAGGAGACAACCTTCCCTTAC	3480
QY	3481	CTGGTAGCATACCAAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCGATCGTGGAC	3540
DB	3481	CTGGTAGCATACCAAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCGATCGTGGAC	3540
QY	3541	CAAAATGTGGAAGTGTCTATACCGCTAAAGCCTACGTCACCGGGCCAAACGCCCTTGCTG	3600
DB	3541	CAAAATGTGGAAGTGTCTATACCGCTAAAGCCTACGTCACCGGGCCAAACGCCCTTGCTG	3600
QY	3601	TATAGGCTGGGAGCCCTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC	3660
DB	3601	TATAGGCTGGGAGCCCTTCAAAACGAGGTTACTACACACACCCCATAAACAAATACATC	3660
QY	3661	ATGGCATGCATGTCCGCTCAGCTCGGAGGTCTGTCACGAGCAGCCTGGTCTATTTGGGCGAGG	3720
DB	3661	ATGGCATGCATGTCCGCTCAGCTCGGAGGTCTGTCACGAGCAGCCTGGTCTATTTGGGCGAGG	3720
QY	3721	GTCCCTAGCAGCTCTGGCCCGTATTGCCTGACAAACGAGCAGCCTGGTCTATTTGGGCGAGG	3780
DB	3721	GTCCCTAGCAGCTCTGGCCCGTATTGCCTGACAAACGAGCAGCCTGGTCTATTTGGGCGAGG	3780
QY	3781	ATCATCTTGTCCGGAAGCCGGCCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTTC	3840
DB	3781	ATCATCTTGTCCGGAAGCCGGCCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTTC	3840
QY	3841	GATGAGATGGAAGTGGCGCTCACACCTTCCCTTACATCGAACAGGGAATGAGCTCGCC	3900
DB	3841	GATGAGATGGAAGTGGCGCTCACACCTTCCCTTACATCGAACAGGGAATGAGCTCGCC	3900
QY	3901	GAAACAAATTCAAACAGAGGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960
DB	3901	GAAACAAATTCAAACAGAGGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960
QY	3961	GCTGCTCCGTTGGGATCCAAAGTGGCGGACCTTCGAAGCCTTCTGGGCGAAGCATATG	4020
DB	3961	GCTGCTCCGTTGGGATCCAAAGTGGCGGACCTTCGAAGCCTTCTGGGCGAAGCATATG	4020
QY	4021	TGGAATTTTCACGCGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGCGAACCCCC	4080
DB	4021	TGGAATTTTCACGCGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGCGAACCCCC	4080
QY	4081	CGGATAGATCACTGATGGCAATTCACAGCCTCTATCACCAGCCGCTCACCACCCCAACAT	4140
DB	4081	CGGATAGATCACTGATGGCAATTCACAGCCTCTATCACCAGCCGCTCACCACCCCAACAT	4140
QY	4141	ACCTCCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCAACTTGCTCTCTCCAGCGCT	4200
DB	4141	ACCTCCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCAACTTGCTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGGGCTGTGGCAGCATAGGCTCTGGG	4260
DB	4201	GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGGGCTGTGGCAGCATAGGCTCTGGG	4260

QY	4261	AAGGTGCTTGAGATAATTTGGGAGGTATGAGCAGGGGTGGCAGGGCGCTGCGGCC	4320	Db	5341	CTGTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTATGACTCCCGGACGCTGAC	5400
Db	4261	AAGGTGCTTGAGATAATTTGGGAGGTATGAGCAGGGGTGGCAGGGCGCTGCGGCC	4320	QY	5401	CTCATCAGGGCAACCTCTCTGTGGCGCAGAGATGGCGGGAACATCACCCGGTGGAG	5460
QY	4321	TTTAAAGTCATGAGGGCGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT	4380	Db	5401	CTCATCAGGGCAACCTCTCTGTGGCGCAGAGATGGCGGGAACATCACCCGGTGGAG	5460
Db	4321	TTTAAAGTCATGAGGGCGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT	4380	QY	5461	TCAGAAATAAGGTAGTAAATTTTGGATCTCTTCGAGCGCTCCAAAGCGGAGGAGATGAG	5520
QY	4381	ATCCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTCGCGAGCGATATGCGTGGCAGC	4440	Db	5461	TCAGAAATAAGGTAGTAAATTTTGGATCTCTTCGAGCGCTCCAAAGCGGAGGAGATGAG	5520
Db	4381	ATCCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTCGCGAGCGATATGCGTGGCAGC	4440	QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGAAATTCCTCGACGATG	5580
QY	4441	GTGGGCCAGAGGAGGGGGCTGTGAGTGATGAACCGGCTGATAGCGTTGCTTCGGGG	4500	Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGAAATTCCTCGACGATG	5580
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QY	4501	GGTAACCAAGTCTCCCGACGCACTATGTCCTGAGAGCGAGCTGACAGCGTGTCACT	4560	Db	5581	CCCATATCGGACGCGCCGATTTACAACTCTCTGTTAGAGTCTCTGGAAGAACCCGGAC	5640
Db	4501	GGTAACCAAGTCTCCCGACGCACTATGTCCTGAGAGCGAGCTGACAGCGTGTCACT	4560	QY	5641	TACGTCCTCTCCAGTGGTACACGGGTGTCCATTCGCGCTGCCAAGGCCCTCCGATACCA	5700
QY	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCCACAGTGAATCAAC	4620	Db	5641	TACGTCCTCTCCAGTGGTACACGGGTGTCCATTCGCGCTGCCAAGGCCCTCCGATACCA	5700
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QY	4621	GAGGACTGCTTCCACGCGCATCTCCGGCTCGTGGCTAAGAGATGTTGGGATGGATATGC	4680	Db	5701	CCTCCACGAGGAGGAGGACGGTGTCTCTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
Db	4621	GAGGACTGCTTCCACGCGCATCTCCGGCTCGTGGCTAAGAGATGTTGGGATGGATATGC	4680	QY	5761	GAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCTCGGCGCTGCACAGCGGCACGGCA	5820
QY	4681	ACGGTCTGACATGATTTCAAGACCTGGCTCAGTCCAAAGCTCTCGCGCGGATTCGCGGA	4740	Db	5761	GAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCTCGGCGCTGCACAGCGGCACGGCA	5820
Db	4681	ACGGTCTGACATGATTTCAAGACCTGGCTCAGTCCAAAGCTCTCGCGCGGATTCGCGGA	4740	QY	5821	ACGGCTCTCTCTGACAGCGCTCCGACGAGCGGAGTCCGAGTCCGAGCTTGAGTCTGATC	5880
QY	4741	GTCCCTCTCTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGCGAGCGCATCATG	4800	Db	5821	ACGGCTCTCTCTGACAGCGCTCCGACGAGCGGAGTCCGAGTCCGAGCTTGAGTCTGATC	5880
Db	4741	GTCCCTCTCTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGCGAGCGCATCATG	4800	QY	5881	TCTTCCATGCCCCCTTGAGGGGAGCGGGGAGTCCCGATCTCAGCGCAGGGCTCTTGG	5940
QY	4801	CAAAACCACTGTCGAGACAGATCACCGGACATGTGAAGACGTTCCATGAGG	4860	Db	5881	TCTTCCATGCCCCCTTGAGGGGAGCGGGGAGTCCCGATCTCAGCGCAGGGCTCTTGG	5940
Db	4801	CAAAACCACTGTCGAGACAGATCACCGGACATGTGAAGACGTTCCATGAGG	4860	QY	5941	TCTTCCATGCCCCCTTGAGGGGAGCGGGGAGTCCCGATCTCAGCGCAGGGCTCTTGG	6000
QY	4861	ATCGTGGGCTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGCGTAC	4920	Db	5941	TCTTCCATGCCCCCTTGAGGGGAGCGGGGAGTCCCGATCTCAGCGCAGGGCTCTTGG	6000
Db	4861	ATCGTGGGCTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGCGTAC	4920	QY	6001	ACAGGGCCCTGTATCAGCCATGCGTGGAGAAACCAAGCTGCCATCAATGCACTG	6060
QY	4921	ACCAAGGGCCCTGCAAGCCCTCCCGCGCGCAAAATTTCTAGGGGCGTGTGGCGGTG	4980	Db	6001	ACAGGGCCCTGTATCAGCCATGCGTGGAGAAACCAAGCTGCCATCAATGCACTG	6060
Db	4921	ACCAAGGGCCCTGCAAGCCCTCCCGCGCGCAAAATTTCTAGGGGCGTGTGGCGGTG	4980	QY	6061	AGCAACTCTTTTGTCTCCGTCACCACTTGTCTATGCTACAACTCTCGCAGCGCAAGC	6120
QY	4981	GCTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTACGTGACGGGCGATG	5040	Db	6061	AGCAACTCTTTTGTCTCCGTCACCACTTGTCTATGCTACAACTCTCGCAGCGCAAGC	6120
Db	4981	GCTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTACGTGACGGGCGATG	5040	QY	6121	CTGGCGCAGAAAGGTCACTTTTGACAGACTGCGAGTCCCTGGAGCACTACCGGGAC	6180
QY	5041	ACCACTGACACGTAAAGTGCCTGTGAGTTCGGGCGCCCGAATTTCTTACAGAAAGTG	5100	Db	6121	CTGGCGCAGAAAGGTCACTTTTGACAGACTGCGAGTCCCTGGAGCACTACCGGGAC	6180
Db	5041	ACCACTGACACGTAAAGTGCCTGTGAGTTCGGGCGCCCGAATTTCTTACAGAAAGTG	5100	QY	6181	GTGCTCAAGGAGTGAAGCGGAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG	6240
QY	5101	GATGGGTGCGGTTCACAGGTACGCTCCAGCGTCAAAACCCCTCTACGGGAGGAGTGC	5160	Db	6181	GTGCTCAAGGAGTGAAGCGGAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG	6240
Db	5101	GATGGGTGCGGTTCACAGGTACGCTCCAGCGTCAAAACCCCTCTACGGGAGGAGTGC	5160	QY	6241	GAGGCTGTAGCTGAGCGCCCACTTCGCGCAGATCTAAATTTTGGCTATGGGCAAG	6300
QY	5161	ACATTCCTGCTGGGCTCAATCAATACCTGGTTCAGCTCCCATGCGAGCCGAA	5220	Db	6241	GAGGCTGTAGCTGAGCGCCCACTTCGCGCAGATCTAAATTTTGGCTATGGGCAAG	6300
Db	5161	ACATTCCTGCTGGGCTCAATCAATACCTGGTTCAGCTCCCATGCGAGCCGAA	5220	QY	6301	GACGTCGCGAACCTATCCAGCAAGCGCTTAAACCATCCGCTCCGTGTGGAGGACTTG	6360
QY	5221	CCGAGCTAGCAGTGTCTACTTCCATGCTCACCGACCCCTCCCATTAACGGCGGAGCG	5280	Db	6301	GACGTCGCGAACCTATCCAGCAAGCGCTTAAACCATCCGCTCCGTGTGGAGGACTTG	6360
Db	5221	CCGAGCTAGCAGTGTCTACTTCCATGCTCACCGACCCCTCCCATTAACGGCGGAGCG	5280	QY	6361	CTGGAAGACACTGTGAGACCAATTTGACACCACTCATGGCAAAATGAGGTTTTCTGC	6420
QY	5281	GCTAAGCGTGGTGGCGGAGGATCTCCCGCTCTTGGCGAGTCTACGTAGCCAG	5340	Db	6361	CTGGAAGACACTGTGAGACCAATTTGACACCACTCATGGCAAAATGAGGTTTTCTGC	6420
Db	5281	GCTAAGCGTGGTGGCGGAGGATCTCCCGCTCTTGGCGAGTCTACGTAGCCAG	5340	QY	6421	GTCCACACAGAGAGGGGGCGGAGCGAGCTCCGCTTATCGTATTCACAGATTGGGG	6480
QY	5341	CTGTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTATGACTCCCGGACGCTGAC	5400				

[illegible]

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RESULT 2
US-09-539-601-7
; Sequence 7, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural protein
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)

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PUBLICATION INFORMATION:

AUTHORS: Lohmann, Volker
AUTHORS: Krner, Frank
AUTHORS: Koch, Jan-Oliver
AUTHORS: Herian, Ulrike
AUTHORS: Theilmann, Lorenz
AUTHORS: Bartenschlager, Ralf
TITLE: Replication of subgenomic hepatitis c virus RNAs in a
TITLE: hepatoma cell line
JOURNAL: Science
VOLUME: 285
PAGES: 110-113
DATE: 1999-07-02
US-09-539-601-7

Query Match 99.7%; Score 7967; DB 4; Length 8001;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 7989; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY	1	GCAGCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTAG	60
Db	1	GCAGCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTAG	60
QY	61	TTTTCAGCAGAAAGCTTAGCCATGGCGTTAGTATGATGTCGACAGCCCTCCAGGAC	120
Db	61	TTTTCAGCAGAAAGCTTAGCCATGGCGTTAGTATGATGTCGACAGCCCTCCAGGAC	120
QY	121	CCCCCTCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGAG	180
Db	121	CCCCCTCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGAG	180
QY	181	GAGCAGCGGTCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGGTGCCCC	240
Db	181	GAGCAGCGGTCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGGTGCCCC	240
QY	241	GCAGAGCTGTAGCCGAGTAGTGTGGTGCAGAAAGCCCTTGTGTACTGCCTGATAG	300
Db	241	GCAGAGCTGTAGCCGAGTAGTGTGGTGCAGAAAGCCCTTGTGTACTGCCTGATAG	300
QY	301	GTGCTTCGAGTGCCCGGAGGTCTGTAGACCGTGCACATGAGCAGAACTCTTAAC	360
Db	301	GTGCTTCGAGTGCCCGGAGGTCTGTAGACCGTGCACATGAGCAGAACTCTTAAC	360
QY	361	CTCAAGAGAAACCAAA-----GGCGCGCATGATTGAACAGATGATTGC	408
Db	361	CTCAAGAGAAACCAAA-----GGCGCGCATGATTGAACAGATGATTGC	420
QY	409	ACGAGGTCTCCGCGCGCTTGGTGGAGAGGTATTCCGCTATGACTGGGCACACAGA	468
Db	421	ACGAGGTCTCCGCGCGCTTGGTGGAGAGGTATTCCGCTATGACTGGGCACACAGA	480
QY	469	CAATCGGTGTCTGATCGCGCGTGTCCGCTGTACGCGAGGGCGCGCGGTCTTT	528
Db	481	CAATCGGTGTCTGATCGCGCGTGTCCGCTGTACGCGAGGGCGCGCGGTCTTT	540
QY	529	TTGTCAAGACCGACTGTCCGCTGATGAATGAATCTGAGACAGGAGCGCGGCTAT	588
Db	541	TTGTCAAGACCGACTGTCCGCTGATGAATGAATCTGAGACAGGAGCGCGGCTAT	600
QY	589	CGTGTGCGCAGAGCGGTCTTGGCAGGTGTGCTCGACGTTGTCACTGAAGCGG	648
Db	601	CGTGTGCGCAGAGCGGTCTTGGCAGGTGTGCTCGACGTTGTCACTGAAGCGG	660
QY	649	GAAAGGACTGGTGTCTTATTTGGGCGAAGTCCCGGGCAGGATCTCTGTCTCATCTT	708
Db	661	GAAAGGACTGGTGTCTTATTTGGGCGAAGTCCCGGGCAGGATCTCTGTCTCATCTT	720
QY	709	CTCTCCGAGAAAGTATCCATCATGCTGATGCGGCGGTGTCATAGCTTGATC	768
Db	721	CTCTCCGAGAAAGTATCCATCATGCTGATGCGGCGGTGTCATAGCTTGATC	780
QY	769	CGGCTACCTGCCCATTTCCAGCCACCAAGCGAAACATCGCATCGAGCGAGACGTACT	828

Db	781	CGGCTACTGCCCCATTGACCAACGAAACATCGCATCGAGCGAGCACGTACTCGGA	840
QY	829	TGGAAGCCGGTCTTTGTCATCAGATGATCTGGACGAAGACATCAGGGCTCGGCCAG	888
Db	841	TGGAAGCCGGTCTTTGTCATCAGATGATCTGGACGAAGACATCAGGGCTCGGCCAG	900
QY	889	CCGAACCTGTCGCAAGGCTCAAGGGCGCATGCCGACGGGAGGATCTCGTCGTGACCC	948
Db	901	CCGAACCTGTCGCAAGGCTCAAGGGCGCATGCCGACGGGAGGATCTCGTCGTGACCC	960
QY	949	ATGGCGATCGCTTGGCGGAATATCATGTGTGGAATAATGGCGCTTTCTGATTCATCG	1008
Db	961	ATGGCGATCGCTTGGCGGAATATCATGTGTGGAATAATGGCGCTTTCTGATTCATCG	1020
QY	1009	ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGTCCCGTGATA	1068
Db	1021	ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGTCCCGTGATA	1080
QY	1069	TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTCTCTGTCTTTACGGTATCGCCG	1128
Db	1081	TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTCTCTGTCTTTACGGTATCGCCG	1140
QY	1129	CTCCGATTCGAGCGCATCGCTTCTATCGCCCTCTTGACGAGTTCTTCTGATTTAAA	1188
Db	1141	CTCCGATTCGAGCGCATCGCTTCTATCGCCCTCTTGACGAGTTCTTCTGATTTAAA	1200
QY	1189	CAGACCAACAGCTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1248
Db	1201	CAGACCAACAGCTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1260
QY	1249	ACGTTACTGGCGGAGCGCTTGAATAGCGCGGTGTCGCTTTGTCTATATGTTATTT	1308
Db	1261	ACGTTACTGGCGGAGCGCTTGAATAGCGCGGTGTCGCTTTGTCTATATGTTATTT	1320
QY	1309	TCACACATATTGCGCTTTTGGCAATGTGAGGCGCCGGAACCTGCGCCCTGTCTTG	1368
Db	1321	TCACACATATTGCGCTTTTGGCAATGTGAGGCGCCGGAACCTGCGCCCTGTCTTG	1380
QY	1369	ACGAGCATTCCTAGGGGTCTTCCCTCTCGCAAGGAATGCAAGCTCTGTTCAATGTC	1428
Db	1381	ACGAGCATTCCTAGGGGTCTTCCCTCTCGCAAGGAATGCAAGCTCTGTTCAATGTC	1440
QY	1429	GTGAAGAGAGCTTCTCTGGAGCTTCTTGAAGACAAACAACTGTAGCGACCCCTT	1488
Db	1441	GTGAAGAGAGCTTCTCTGGAGCTTCTTGAAGACAAACAACTGTAGCGACCCCTT	1500
QY	1489	TGCAGGAGCGGAACCCCGACCTTGGCGACAGGTGCTCTCGGCGCAAAAGCCAGTGA	1548
Db	1501	TGCAGGAGCGGAACCCCGACCTTGGCGACAGGTGCTCTCGGCGCAAAAGCCAGTGA	1560
QY	1549	TAAGATACACTGCAAGGCGGCAACCCAGTGCACAGTGTGAGTTGATAGTTCTG	1608
Db	1561	TAAGATACACTGCAAGGCGGCAACCCAGTGCACAGTGTGAGTTGATAGTTCTG	1620
QY	1609	GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGAGTCCGAGAG	1668
Db	1621	GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGAGTCCGAGAG	1680
QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGTTTACATGTTTAG	1728
Db	1681	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGTTTACATGTTTAG	1740
QY	1729	TCGAGTTTAAAAAAGTCTAGGCCCGGACCAAGGAGCTGTTTCTTGAATAA	1788
Db	1741	TCGAGTTTAAAAAAGTCTAGGCCCGGACCAAGGAGCTGTTTCTTGAATAA	1800
QY	1789	CAAGATATACCATGCGGCTATTACGGCTACTCCCAACAGACGCGAGGCTTCTGCG	1848
Db	1801	CAAGATATACCATGCGGCTATTACGGCTACTCCCAACAGACGCGAGGCTTCTGCG	1860
QY	1849	TGCATCATCACTAGCTCTCAGCGCGGACAGGAACAGGTCGAGGGGAGGTCCAGTG	1908
Db	1861	TGCATCATCACTAGCTCTCAGCGCGGACAGGAACAGGTCGAGGGGAGGTCCAGTG	1920

1909 GTCTCCACCGCACAAATCTTTCTGGGACCTGGTCAATGGCGGTGTTGGAGTGC 1968
1921 GTCTCCACCGCACAAATCTTTCTGGGACCTGGTCAATGGCGGTGTTGGAGTGC 1980
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1981 TATCATGGTGGCGGCTCAAAAGACCTTTGCCGGCCCAAGAGGCCCAATCACCCAAATGTAC 2040
2029 ACCAATGTGGACAGAACCTGTGGCTGGCAAGCGCCCCCGGGGCGGTCTCTTGACA 2088
2041 ACCAATGTGGACAGAACCTGTGGCTGGCAAGCGCCCCCGGGGCGGTCTCTTGACA 2100
2089 CCATGCACTCGCGGAGCTCGGACCTTTACTTTGTTGTCACAGGAGATGCCGATGTCAATCCG 2148
2101 CCAATGCACTCGCGGAGCTCGGACCTTTACTTTGTTGTCACAGGAGATGCCGATGTCAATCCG 2160
2149 GTGCGCGCGGGGGGACAGCAGAGGGGAGCCTACTCTCCCGGAGCGCTGTGGGCACTCTTTCGG 2208
2161 GTGCGCGCGGGGGGACAGCAGAGGGGAGCCTACTCTCCCGGAGCGCTGTGGGCACTCTTTCGG 2220
2209 AAGGGCTCTTGGGGGGTCCACTGTCTGCCCTCGGGGACAGCTGTGGGCACTCTTTCGG 2268
2221 AAGGGCTCTTGGGGGGTCCACTGTCTGCCCTCGGGGACAGCTGTGGGCACTCTTTCGG 2280
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2341 GAAACCACTATGCGGTCCCGGCTTTACAGGACAACTCGTCTGCCCGGCGTACCTGAGTCTATG 2400
2389 ACATTCAGGTGGCCCATCTACCGCCCTACTGTAGCGGCAAGACACTAAGTGTCCG 2448
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2869 ATCGAGACCATCAAGGGGGGAGGACCTTCATTTCTGCGCATTCAGAAAGAAATGTGAT 2928
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3109 GTGCACTTCAGCTCGGACCCGACCTTACCATTTGAGACGACGACCTGCCACAGAGCGG 3168
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3169 GTGTCACTCGCAGCGGCGAGGAGGACTGTAGGGCAGGATGGGCAATTTACAGGTTT 3228
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Qy	6289	TATGGGGCAAGGACGTCCGGAAACCTATCCAGCAAGGCCGTTAACCACTCCGCTCCGTG	6348
Db	6301	TATGGGGCAAGGACGTCCGGAAACCTATCCAGCAAGGCCGTTAACCACTCCGCTCCGTG	6360
Qy	6349	TGGAAGNACTTGCTGGAAAGACACTGAGACACCAATTGACACCACTATGGCAAAAAAT	6408
Db	6361	TGGAAGNACTTGCTGGAAAGACACTGAGACACCAATTGACACCACTATGGCAAAAAAT	6420
Qy	6409	GAGGTTTTCTCGCTCCAACACAGAAAGGGGGCGCAAGCCAGCTCGCTTATGCTATTC	6468
Db	6421	GAGGTTTTCTCGCTCCAACACAGAAAGGGGGCGCAAGCCAGCTCGCTTATGCTATTC	6480
Qy	6469	CCAGATTTGGGGTTCGTGTGCGAGAAATGGCCCTTTACGATGTGCTCCACCCCTC	6528
Db	6481	CCAGATTTGGGGTTCGTGTGCGAGAAATGGCCCTTTACGATGTGCTCCACCCCTC	6540
Qy	6529	CCTCAGCCGTGATGGGCTCTTCAATCGGAATCCAAATPACTCTCTCGGACAGCGGTCGAG	6588
Db	6541	CCTCAGCCGTGATGGGCTCTTCAATCGGAATCCAAATPACTCTCTCGGACAGCGGTCGAG	6600
Qy	6589	TTCTCGTGAATGCCTCGAAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCG	6648
Db	6601	TTCTCGTGAATGCCTCGAAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCG	6660
Qy	6649	TGTTTTGACTCAACGGTCACTGAGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGT	6708
Db	6661	TGTTTTGACTCAACGGTCACTGAGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGT	6720
Qy	6709	TGTGACTTGGCCCCCGAAGCCAGACAGGCCTAAGGTTCGTCTCAGAGCGGCTTACATC	6768
Db	6721	TGTGACTTGGCCCCCGAAGCCAGACAGGCCTAAGGTTCGTCTCAGAGCGGCTTACATC	6780
Qy	6769	GGGGGCCCCCTGACTAAATCTTAAAGGCGCAACTGCGGCTATCGCGGTCCGCGCGAGC	6828
Db	6781	GGGGGCCCCCTGACTAAATCTTAAAGGCGCAACTGCGGCTATCGCGGTCCGCGCGAGC	6840
Qy	6829	GGTGTACTGACACCAAGCTGCGGTAATACCTCACATGTTTACTTGAAGCGCGTCGCGCC	6888
Db	6841	GGTGTACTGACACCAAGCTGCGGTAATACCTCACATGTTTACTTGAAGCGCGTCGCGCC	6900
Qy	6889	TGTCGAGCTTGGAAAGCTCCAGGACTGCAAGATCTCGTATCGGAGACGACCTTGTGCTT	6948
Db	6901	TGTCGAGCTTGGAAAGCTCCAGGACTGCAAGATCTCGTATCGGAGACGACCTTGTGCTT	6960
Qy	6949	ATCTGTGAAGCGGGGACCCAAAGAGACGAGGCGAGCCTACGGGCTTACAGGAGCT	7008
Db	6961	ATCTGTGAAGCGGGGACCCAAAGAGACGAGGCGAGCCTACGGGCTTACAGGAGCT	7020
Qy	7009	ATGACTAGATACTCTGCCCCCTCGGGACCGCCCAACACAGAAATACGACTTGCAGTTG	7068
Db	7021	ATGACTAGATACTCTGCCCCCTCGGGACCGCCCAACACAGAAATACGACTTGCAGTTG	7080
Qy	7069	ATAACATCATGCTCTCCAAATGTGTCAGTCGGGCAAGATGCAATCTGGCAAGGGTGTAC	7128
Db	7081	ATAACATCATGCTCTCCAAATGTGTCAGTCGGGCAAGATGCAATCTGGCAAGGGTGTAC	7140
Qy	7129	TATCTCACCCGTGACCCCAACCCCTTTCGCGGGCTGGGTGGGACAGCTAGACAC	7188
Db	7141	TATCTCACCCGTGACCCCAACCCCTTTCGCGGGCTGGGTGGGACAGCTAGACAC	7200
Qy	7189	ACTCAGTCAATTCCTGGCTAGGCAACATCATGTATGCGCCCACTTGTGGGCAAGG	7248
Db	7201	ACTCAGTCAATTCCTGGCTAGGCAACATCATGTATGCGCCCACTTGTGGGCAAGG	7260
Qy	7249	ATGATCCTGATCACTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCC	7308
Db	7261	ATGATCCTGATCACTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCC	7320
Qy	7309	CTAGATTGTGACATCTACGGGCGCTTACTCCATTTAGGCCACTTGACCTACCTAGATC	7368
Db	7321	CTAGATTGTGACATCTACGGGCGCTTACTCCATTTAGGCCACTTGACCTACCTAGATC	7380

QY	7369	ATTCAAGCACTCCATGCGCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATC	7429
DB	7381	ATTCAACGACTCCATGCGCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATC	7440
QY	7429	AATAGGTGGCTTCATCGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7488
DB	7441	AATAGGTGGCTTCATCGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7500
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DB	7501	CGGCGCAGAGTGTCCGCGCTAGGCTACTGTCCCGAGGGGGAGGGCTGCCACTTTGTGGC	7560
QY	7549	AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGG	7608
DB	7561	AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGG	7620
QY	7609	TCCCAGTTGGAATTAATCAGCTGGTTCTGTTGTGTTTACAGGGGGAGACATATATCAC	7668
DB	7621	TCCCAGTTGGAATTAATCAGCTGGTTCTGTTGTGTTTACAGGGGGAGACATATATCAC	7680
QY	7669	AGCCTGTCTCGTGGCCGACCCGCTGCTTCATGTGTGCTACTCCTACTTTCTGTAGGG	7728
DB	7681	AGCCTGTCTCGTGGCCGACCCGCTGCTTCATGTGTGCTACTCCTACTTTCTGTAGGG	7740
QY	7729	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGG	7788
DB	7741	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGG	7800
QY	7789	CCATCCGTGTTTTTTTCCCTT	7848
DB	7801	CCATCCGTGTTTTTTTCCCTT	7860
QY	7849	TTTTTCTCCTTTTTTTTTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7908
DB	7861	TTTTTCTCCTTTTTTTTTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7920
QY	7909	CCTAGTCAAGGCTAGCTGTGAAGGTCCGTGAGCCGCTTTGACTGCAGAGAGTCTGTATAC	7968
DB	7921	CCTAGTCAAGGCTAGCTGTGAAGGTCCGTGAGCCGCTTTGACTGCAGAGAGTCTGTATAC	7980
QY	7969	TGGCCTCTCTGCAGATCAAGT	7989
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RESULT 3

US-09-539-601-22

; Sequence 22, Application US/09539601C

; Patent No. 6630343

; GENERAL INFORMATION:

; APPLICANT: Bartenschlager, Ralf FW

; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System

; FILE REFERENCE: all sequences

; CURRENT APPLICATION NUMBER: US/09/539,601C

; CURRENT FILING DATE: 2001-08-30

; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

; EARLIER FILING DATE: 1999-04-03

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 22

; LENGTH: 8001

; TYPE: DNA

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: (1)..(341)

; OTHER INFORMATION: construct I389/NS3-3'/5.1

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (342)..(1193)

; OTHER INFORMATION: hepatitis C virus core - neomycin

; OTHER INFORMATION: phosphotransferase fusion protein

; FEATURE:

NAME/KEY: RBS
LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(7770)
OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
OTHER INFORMATION: of cell culture-adapted clone no. 5.1
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (7771)..(8001)
US-09-539-601-22

Query Match 99.5%; Score 7949.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7978; Conservative 0; Mismatches 11; Indels 12; Gaps 1;

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QY 61 TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTGTCGACGCTCCAGGAC 120
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QY 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAAATTGCCAG 180
Db 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAAATTGCCAG 180

QY 181 GAGCAGCGGTCTTTCTTGGATCAACCGCTCAATGCCCTGGAGATTGGCGGTGCCGCC 240
Db 181 GAGCAGCGGTCTTTCTTGGATCAACCGCTCAATGCCCTGGAGATTGGCGGTGCCGCC 240

QY 241 GCAGAGTGTACCGAGTAGTGTGGGTGCGAAAGGCTTGTGTAAGTCTGCTGATAG 300
Db 241 GCAGAGTGTACCGAGTAGTGTGGGTGCGAAAGGCTTGTGTAAGTCTGCTGATAG 300

QY 301 GTGCTTTCGAGTCCCGGAGGTCTGCTGAGACCGGTGACACCATGAGCAGAACTCTAAC 360
Db 301 GTGCTTTCGAGTCCCGGAGGTCTGCTGAGACCGGTGACACCATGAGCAGAACTCTAAC 360

QY 361 CTCAAAGAAAACCAA-----GGGCGCGCATGATTGAACAAGATGGATTGC 408
Db 361 CTCAAAGAAAACCAAACCAACGCGGCGCGCCATGATGAACAAGATGGATTGC 420

QY 409 ACGCAGTCTTCGCGCGCTTGGGTGAGAGGCTATTCCGCTATGATGTCGGCAACAAGA 468
Db 421 ACGCAGTCTTCGCGCGCTTGGGTGAGAGGCTATTCCGCTATGATGTCGGCAACAAGA 480

QY 469 CAATCGGCTGCTGATGCGCGCTGTTCCGCTGTGAGCGAGGGCGCGGTTCTTT 528
Db 481 CAATCGGCTGCTGATGCGCGCTGTTCCGCTGTGAGCGAGGGCGCGGTTCTTT 540

QY 529 TTGTCAGACCGACTCTCGGTGCTGATGAATGAATGACGAGCAGCGCGGCTAT 588
Db 541 TTGTCAGACCGACTCTCGGTGCTGATGAATGAATGACGAGCAGCGCGGCTAT 600

QY 589 CGTGGCTGGCCACGACGGCGCTTCCTTCCGAGTGTGTCGAGTGTGTCATGAGGCG 648
Db 601 CGTGGCTGGCCACGACGGCGCTTCCTTCCGAGTGTGTCGAGTGTGTCATGAGGCG 660

QY 649 GAAGGACTGCTGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCATCTCACCTTG 708
Db 661 GAAGGACTGCTGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCATCTCACCTTG 720

QY 709 CTCCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGTGATACGCTTGATC 768
Db 721 CTCCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGTGATACGCTTGATC 780

QY 769 CGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCATGAGCGGACGCTACTCGGA 828
Db 781 CGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCATGAGCGGACGCTACTCGGA 840

QY 829 TGAAGCGCGTCTTTGTCGATCAGGATGATCTGAGAGAGATCATCGGGCTCGGGCAG 888
Db 841 TGAAGCGCGTCTTTGTCGATCAGGATGATCTGAGAGAGATCATCGGGCTCGGGCAG 900

QY 889 CCGAACTGTTCCGAGGCTCAAGGGCGCATGCCGACGGGAGGATCTCTGTCGTGACCC 948
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Dd	4081	CCTGGCAACCCCGGATAGCATCACTGATGCGATTCACAGCCTCTATCACCGACCGCGTC	4140	Qy	5209	TGCGAGCCCGAACCGGACGTAGCAGTGTCTCATCTTCCATGCTCACCGACCCCTCCCAATT	5268
Qy	4129	ACCAACCAACATACCTCTCTGTTTAAACATCCTGGGGGATGGGTGGCCGCCCAACTTGCT	4188	Dd	5221	TGCGAGCCCGAACCGGATGATGCTCATCTTCCATGCTCACCGACCCCTCCCAATT	5280
Dd	4141	ACCAACCAACATACCTCTCTGTTTAAACATCCTGGGGGATGGGTGGCCGCCCAACTTGCT	4200	Qy	5269	ACGGCGGAGAGCGGTAAAGCTAGGTGGCCAGGGGATCTCCGCCCTCTCTGGCCAGCTCA	5328
Qy	4189	CCTCCAGCGTGTCTTCTGCTTCTGCTAGCGCCGCGATCGCTGGAGCGGCTGTTGGCAGC	4248	Dd	5281	ACGGCGGAGAGCGGTAAAGCTAGGTGGCCAGGGGATCTCTCCGCCCTCTGGCCAGCTCA	5340
Dd	4201	CCTCCAGCGTGTCTTCTGCTTCTGCTAGCGCCGCGATCGCTGGAGCGGCTGTTGGCAGC	4260	Qy	5329	TCAGTACCCAGCTGTCTGCGCCTTCTTGAAGGCAACATGCACTACCGCTCATGACTCC	5388
Qy	4249	ATAGCCCTGGGAAGTCTCTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGGC	4308	Dd	5341	TCAGTACCCAGCTGTCTGCGCCTTCTTGAAGGCAACATGCACTACCGCTCATGACTCC	5400
Dd	4261	ATAGCCCTGGGAAGTCTCTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGGC	4320	Qy	5389	CCGACGCTGACCTCATCGAGCCCAACCTCTCTGTCGGCGGAGAGATGGCGGGAGACATC	5448
Qy	4309	GCGCTCTGGGCCCTTAAAGTCTATGAGCGCGAGATGCCCTCCACCGAGACCTGTTAAC	4368	Dd	5401	CCGACGCTGACCTCATCGAGCCCAACCTCTCTGTCGGCGGAGAGATGGCGGGAGACATC	5460
Dd	4321	GCGCTCTGGGCCCTTAAAGTCTATGAGCGCGAGATGCCCTCCACCGAGACCTGTTAAC	4380	Qy	5449	ACCGCGTGGAGTCAGAAATAAGGTAGTAAATTTTGGACTCTTTGAGCGGCTTCAAAGCG	5508
Qy	4369	CTACTCCCTGTCTATCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTGGCGCGGATA	4428	Dd	5461	ACCGCGTGGAGTCAGAAATAAGGTAGTAAATTTTGGACTCTTTGAGCGGCTTCAAAGCG	5520
Dd	4381	CTACTCCCTGTCTATCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTGGCGCGGATA	4440	Qy	5509	GAGGAGATGAGAGGAAGTATCCGTTCCGGCGGAGATCCTGCGAGGTCAGGAAATTC	5568
Qy	4429	CTGGCTCGGACGTGGGCCAGGGAGGGGCTGTGACGTGGATGAACCGGCTGATAGCG	4488	Dd	5521	GAGGAGATGAGAGGAAGTATCCGTTCCGGCGGAGATCCTGCGAGGTCAGGAAATTC	5580
Dd	4441	CTGGCTCGGACGTGGGCCAGGGAGGGGCTGTGACGTGGATGAACCGGCTGATAGCG	4500	Qy	5569	CCTCGAGCGATGCCATATGGGCACGCCCGGATTACAACTCTCACTGTAGAGTCTTG	5628
Qy	4489	TTTCCTTCGGGGGTAAACCACTCTCCCGACGCACTATGTGCTGAGAGCGCTGCA	4548	Dd	5581	CCTCGAGCGATGCCATATGGGCACGCCCGGATTACAACTCTCACTGTAGAGTCTTG	5640
Dd	4501	TTTCCTTCGGGGGTAAACCACTCTCCCGACGCACTATGTGCTGAGAGCGCTGCA	4560	Qy	5629	MAGGACCGGACTACGCTCCCTCCAGTGTACAGGGTGTCCATTGCGGCTTCAAAGGCC	5688
Qy	4549	GCAGTGTCACTCAGATCTCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTAC	4608	Dd	5641	MAGGACCGGACTACGCTCCCTCCAGTGTACAGGGTGTCCATTGCGGCTTCAAAGGCC	5700
Dd	4561	GCAGTGTCACTCAGATCTCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTAC	4620	Qy	5689	CCTCCGATACCACTCCACCGGAGAGAGGACGGTGTCTGTGTCAGATCTACGCTGTCT	5748
Qy	4609	CAGTGGATCAACGAGGACTCTCCACGCCATGTCTCGGCTCTGCTGCTGAAGATGTTGG	4668	Dd	5701	CCTCCGATACCACTTTCAGGAGAGAGGACGGTGTCTGTGTCAGATCTACGCTGTCT	5760
Dd	4621	CAGTGGATCAACGAGGACTCTCCACGCCATGTCTCGGCTCTGCTGCTGAAGATGTTGG	4680	Qy	5749	TTTCCTTCGGGAGCTCGGCAACAGACCTTCCGAGCTTCCGAATCGTGGCGCTCGAC	5808
Qy	4669	GATTGGATATGCAAGGTGTTGACTGATTTCAAGACCTTGGCTCCAGTCCCAAGCTCTCCG	4728	Dd	5761	TTTCCTTCGGGAGCTCGGCAACAGACCTTCCGAGCTTCCGAATCGTGGCGCTCGAC	5820
Dd	4681	GATTGGATATGCAAGGTGTTGACTGATTTCAAGACCTTGGCTCCAGTCCCAAGCTCTCCG	4740	Qy	5809	AGCGGACGCAACGGCTCTCTGACAGCCCTCCGACGCGCTCCGACGCGGAGATCCGAC	5868
Qy	4729	CGATTGCGGGAGTCCCTCTCTCTCTCATGTCAAGTGGTACAGGGAGTCTGGCGGGC	4788	Dd	5821	AGCGGACGCAACGGCTCTCTGACAGCCCTCCGACGCGCTCCGACGCGGAGATCCGAC	5880
Dd	4741	CGATTGCGGGAGTCCCTCTCTCTCTCATGTCAAGTGGTACAGGGAGTCTGGCGGGC	4800	Qy	5869	GTTGAGTGTACTCTCTCCATGCCCTTTAGGGGAGGCGGGGATCCCGATCTCAGC	5928
Qy	4789	GACGGCATATGCAAAACCACTGCGCCATGTGGAGCAGACATCACCGGACATGTGAAAAAC	4848	Dd	5881	GTTGAGTGTACTCTCTCCATGCCCTTTAGGGGAGGCGGGGATCCCGATCTCAGC	5940
Dd	4801	GACGGCATATGCAAAACCACTGCGCCATGTGGAGCAGACATCACCGGACATGTGAAAAAC	4860	Qy	5929	GACGGCTTTGGTCTACCGTAAGCGAGAGGCTAGTGGAGGACGTCTGCTGCTCGATG	5988
Qy	4849	GGTTCCATGAGGATCGTGGGCGCTTAGGACCTGTAGTAAACAGTGGCATGGAACTTCCC	4908	Dd	5941	GACGGCTTTGGTCTACCGTAAGCGAGAGGCTAGTGGAGGACGTCTGCTGCTCGATG	6000
Dd	4861	GGTTCCATGAGGATCGTGGGCGCTTAGGACCTGTAGTAAACAGTGGCATGGAACTTCCC	4920	Qy	5989	TCCTACACATGACAGGCGGCTCATACGCGCATGCTGCGGAGGAAACCAAGTGGCC	6048
Qy	4909	ATTAAACGGGTACACACGGGCGCTGACGCGCTCCCGCGGCCAAATTTATTTAGGGCG	4968	Dd	6001	TCCTACACATGACAGGCGGCTCATACGCGCATGCTGCGGAGGAAACCAAGTGGCC	6060
Dd	4921	ATTAAACGGGTACACACGGGCGCTGACGCGCTCCCGCGGCCAAATTTATTTAGGGCG	4980	Qy	6049	ATCAATGACATGAGCACTCTTTGCTCCGTCCACCAAACTTGGTCTATGCTACAACTCT	6108
Qy	4969	CTGTGGGGGTGGTGTCTGAGGAGTACGTTGAGGTTTACCGGGTGGGGATTTCCACTAC	5028	Dd	6061	ATCAATGACATGAGCACTCTTTGCTCCGTCCACCAAACTTGGTCTATGCTACAACTCT	6120
Dd	4981	CTGTGGGGGTGGTGTCTGAGGAGTACGTTGAGGTTTACCGGGTGGGGATTTCCACTAC	5040	Qy	6109	CGCAGCGCAAGCTGCGGACAGAGGCTCACTTTGACAGCTCAGGCTCTCGGACGAC	6168
Qy	5029	GTGACGGGATGACCACTGACAAAGTAAAGTCCCGTGTGAGGTTCCGGCCCCCAATTC	5088	Dd	6121	CGCAGCGCAAGCTGCGGACAGAGGCTCACTTTGACAGCTCAGGCTCTCGGACGAC	6180
Dd	5041	GTGACGGGATGACCACTGACAAAGTAAAGTCCCGTGTGAGGTTCCGGCCCCCAATTC	5100	Qy	6169	CACTACCGGAGCTGCTCAAGGAGATGAAGGCGAAGGGCTCCAGTTAAGGCTAAACTT	6228
Qy	5089	TTTACAGAGTGGATGGGCTGGGTGACAGGTACGTTCCAGCGGTGCAAAACCCCTCTTA	5148	Dd	6181	CACTACCGGAGCTGCTCAAGGAGATGAAGGCGAAGGGCTCCAGTTAAGGCTAAACTT	6240
Dd	5101	TTTACAGAGTGGATGGGCTGGGTGACAGGTACGTTCCAGCGTCCAGCGGTGCAAAACCCCTCTTA	5160	Qy	6229	CTATCCGTGGAGGAGCTGTAAAGCTGACCGCCCCACATTGGCCAGATCTAAATTTGGC	6288
Qy	5149	CGGGAGGAGGTCACTTCCTGTGGGTGGGCTCAATCAATACCTGGTGGGTCAAGCTCCCA	5208	Dd	6241	CTATCCGTGGAGGAGCTGTAAAGCTGACCGCCCCACATTTCGGCCAGATCTAAATTTGGC	6300
Dd	5161	CGGGAGGAGGTCACTTCCTGTGGGTGGGCTCAATCAATACCTGGTGGGTCAAGCTCCCA	5220				

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7981 TGGCCTCTCTGCAGATCAAGT 8001

RESULT 4

US-09-539-601-16
; Sequence 16, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; EARLIER FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/9-13F
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS

LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(7770)
OTHER INFORMATION: hepatitis C virus nonstructural protein NS3-5B;
OTHER INFORMATION: carries cell culture-adaptive mutations from clone
OTHER INFORMATION: 9-13F
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (7771)..(8001)
US-09-539-601-16

Query Match 99.4%; Score 7947.8; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7977; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 1 GCAGGCCCGGATGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60
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Db 61 TCTTACGACAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC 120

QY 121 CCCCCCTCCGGAGAGCCATAGTGTCTGCGGAAACGGGTGAGTACACCGGAATTGCCAG 180
Db 121 CCCCCCTCCGGAGAGCCATAGTGTCTGCGGAAACGGGTGAGTACACCGGAATTGCCAG 180

QY 181 GAGCAGCGGTCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCCC 240
Db 181 GAGCAGCGGTCTTTCTTGATCAACCCGCTCAATGCCCTGGAGATTGGCGCTGCCCCC 240

QY 241 GCAGACTGTACCGAGTAGTGTGGGTGCGAAAGCGCTTGTGTTACTGCTCTGATAG 300
Db 241 GCAGACTGTACCGAGTAGTGTGGGTGCGAAAGCGCTTGTGTTACTGCTCTGATAG 300

QY 301 GTCTTTCGAGTCCCGGAGGTCTGTTAGACCGGTGACACCGCGCGCCATGACCAATCCTAAC 360
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QY 361 CTCAAGAAACCAAA-----GGGCGCGCATGATTGAACAAGATGGATTGC 408
Db 361 CTCAAGAAACCAAA-----GGGCGCGCATGATTGAACAAGATGGATTGC 408

QY 409 ACGCAGGTCTTCGGCGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAAGA 468
Db 409 ACGCAGGTCTTCGGCGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAAGA 468

QY 469 CAATCGGCTGTCTGATGCGCGCGTGTTCGGCTGTGAGCGGCGGCGCGGCTCTTT 528
Db 469 CAATCGGCTGTCTGATGCGCGCGTGTTCGGCTGTGAGCGGCGGCGCGGCTCTTT 528

QY 529 TTGTCAAGACCGACTGTCCGCTGCTGAATGAATGCAATGCAAGCGAGCGCGGCTAT 588
Db 529 TTGTCAAGACCGACTGTCCGCTGCTGAATGAATGCAATGCAAGCGAGCGCGGCTAT 588

QY 541 TTGTCAAGACCGACTGTCCGCTGCTGAATGAATGCAATGCAAGCGAGCGCGGCTAT 600
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QY 721 CTCCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGCATACGTTGATC 780
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QY 769 CGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGGAGCACTACTCGGA 828
Db 769 CGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGGAGCACTACTCGGA 828

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Db 841 TGAAGCCGGTCTTGTGATCAGATGATCTGACGAAGAGCATCAGGGGTGCGGCCAG 900

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Db 961 ATGGGATGCTGCTTGGCGGATATCATGGTGGAAATGGCGCTTTCTGATTCATCG 1020

QY 1009 ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTGTGGCTACCCGTCATA 1068
Db 1021 ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTGTGGCTACCCGTCATA 1080

QY 1069 TTGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTTCTCGTGTCTTACGCTATCGCG 1128
Db 1081 TTGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTTCTCGTGTCTTACGCTATCGCG 1140

QY 1129 CTCGCGATTCGAGCGCATCGCTTCTATCGGCTTCTTGACGAGTTCCTTCTGATTTAA 1188
Db 1141 CTCGCGATTCGAGCGCATCGCTTCTATCGGCTTCTTGACGAGTTCCTTCTGATTTAA 1200

QY 1189 CAGACCAACAGCTTCCCTCTAGCGGATCAATTCGCGGCTTCTCCCTCCCGCCCT 1248
Db 1201 CAGACCAACAGCTTCCCTCTAGCGGATCAATTCGCGGCTTCTCCCTCCCGCCCT 1260

QY 1249 AACGTTACTGGCGAAGCGCTTGAATGAAGCGGCTGCGCTTCTCTATATGTTATTT 1308
Db 1261 AACGTTACTGGCGAAGCGCTTGAATGAAGCGGCTGCGCTTCTCTATATGTTATTT 1320

QY 1309 TCCACCATATGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTGCTCTTTG 1368
Db 1321 TCCACCATATGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTGCTCTTTG 1380

QY 1369 ACAGCATTCCTAGGGGTCTTCCCTCTGCGCAAGGATGCAAGTCTGTTGAATGTC 1428
Db 1381 ACAGCATTCCTAGGGGTCTTCCCTCTGCGCAAGGATGCAAGTCTGTTGAATGTC 1440

QY 1429 GTGAAGAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTGTGAGCGACCTT 1488
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QY 1489 TGAGGCGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGGCCAAAAGCCACGTGA 1548
Db 1501 TGAGGCGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGGCCAAAAGCCACGTGA 1560

QY 1549 TAAAGATACACCTGCAAGGGCGGCAACCCCGACAGTTCGTCAGTGTGATGTTGTTG 1608
Db 1561 TAAAGATACACCTGCAAGGGCGGCAACCCCGACAGTTCGTCAGTGTGATGTTGTTG 1620

QY 1609 GAAAGATCAATAGGCTCTCTCAAGGCTATTCAAGGGGCTGAAGGATGCCAGAAAG 1668
Db 1621 GAAAGATCAATAGGCTCTCTCAAGGCTATTCAAGGGGCTGAAGGATGCCAGAAAG 1680

QY 1669 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGTTACATGTTTGTAG 1728
Db 1681 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGTTACATGTTTGTAG 1740

QY 1729 TCGAGGTTAAAGAGCTTAGGCCCGCGAACCACGCGGAGCTGGTTTCTTTTGAAGAA 1788
Db 1741 TCGAGGTTAAAGAGCTTAGGCCCGCGAACCACGCGGAGCTGGTTTCTTTTGAAGAA 1800

QY 1789 CACGATTAACCATGGCGCTATTACGCGCTTCTCCAAACAGACGAGGCTTACTTGGC 1848
Db 1801 CACGATTAACCATGGCGCTATTACGCGCTTCTCCAAACAGACGAGGCTTACTTGGC 1860

QY 1849 TGCATCATCACTAGCTTCAAGCGCGGACAGGAACCAAGTTCGAGGGGAGGTCCAAAGTG 1908
Db 1861 TGCATCATCACTAGCTTCAAGCGCGGACAGGAACCAAGTTCGAGGGGAGGTCCAAAGTG 1920

QY	1909	GTCTCCACCGCAACA	CAATCTTTCTTGGCGAC	CGTGGTCAATGCGCGTGTGTTGCACTGTC	196
Db	1921	GTCTCCACCGCAACA	CAATCTTTCTTGGCGAC	CGTGGTCAATGCGCGTGTGTTGCACTGTC	1980
QY	1969	TATCATGTGCGGGCTCA	AAAGACCCTTGGCGGCC	MAAGGGGCCAATCAACCCAAATGTAC	2028
Db	1981	TATCATGTGCGGGCTCA	AAAGACCCTTGGCGGCC	MAAGGGGCCAATCAACCCAAATGTAC	2040
QY	2029	ACCAATGTGACACGAG	CACTGTCGGCTGGCAAG	CGCCCCCGGGGGCGTTCCTTGACA	2088
Db	2041	ACCAATGTGACACGAG	CACTGTCGGCTGGCAAG	CGCCCCCGGGGGCGTTCCTTGACA	2100
QY	2089	CCATGCACTTCGGGAG	CTCGGACTTTTAC	TGGTCAAGAGCATGCGCATCTTCG	2148
Db	2101	CCATGCACTTCGGGAG	CTCGGACTTTTAC	TGGTCAAGAGCATGCGCATCTTCG	2160
QY	2149	GTGCGCGGGGGCGCAG	CAGCAGGGGAGCCTACT	CTCCCCCAGGGCCGTCTCTCTACTTTG	2208
Db	2161	GTGCGCGGGGGCGCAG	CAGCAGGGGAGCCTACT	CTCCCCCAGGGCCGTCTCTCTACTTTG	2220
QY	2209	AAGGGCTCTTCGGGCG	GTCCAATGCTCTGCCCC	CTCGGGGCAAGCTGTGGGCATCTTCGG	2268
Db	2221	AAGGGCTCTTCGGGCG	GTCCAATGCTCTGCCCC	CTCGGGGCAAGCTGTGGGCATCTTCGG	2280
QY	2269	GCTGCGGTGTGCAC	CCGAGGGGTTGGAAG	CGGTGGACTTTGTACCGTCTGAGTCTATG	2328
Db	2281	GCTGCGGTGTGCAC	CCGAGGGGTTGGAAG	CGGTGGACTTTGTACCGTCTGAGTCTATG	2340
QY	2329	GAACCACTATGCGGT	CCCCCGTCTTCAAGCA	CAACTCGTCCCCCTCGAGTCTATG	2388
Db	2341	GAACCACTATGCGGT	CCCCCGTCTTCAAGCA	CAACTCGTCCCCCTCGAGTCTATG	2400
QY	2389	ACATTCAGGTGCCCC	ATCTACAGCCCCCTACT	GCTAGCGGCAAGACACTAAAGTGGCG	2448
Db	2401	ACATTCAGGTGCCCC	ATCTACAGCCCCCTACT	GCTAGCGGCAAGACACTAAAGTGGCG	2460
QY	2449	GCTGCGTATGCAGC	CCCAAGGGTATAGGT	GTGCTCTGAAACCGTCTCGCGCCGACCC	2508
Db	2461	GCTGCGTATGCAGC	CCCAAGGGTATAGGT	GTGCTCTGAAACCGTCTCGCGCCGACCC	2520
QY	2509	CTAGGTTTCGGGCGT	ATATGCTTAGGCA	CATGGTATCGACCTTACATCAGAACCGGG	2568
Db	2521	CTAGGTTTCGGGCGT	ATATGCTTAGGCA	CATGGTATCGACCTTACATCAGAACCGGG	2580
QY	2569	GTAAAGCAATCACA	CGGGTGCCCGCATCA	CGCTACTCCACCTATGCAAGTCTTCTGCC	2628
Db	2581	GTAAAGCAATCACA	CGGGTGCCCGCATCA	CGCTACTCCACCTATGCAAGTCTTCTGCC	2640
QY	2629	GACGTGTGTGCTCT	TGGGGCGGCTATG	ATATATGTGATGAGTGCCTCAACT	2688
Db	2641	GACGTGTGTGCTCT	TGGGGCGGCTATG	ATATATGTGATGAGTGCCTCAACT	2700
QY	2689	GACTCGACCACTAT	CTCTGGGCATCGCA	CAGTCTGCAACGGGAGACGGCTGGAGCG	2748
Db	2701	GACTCGACCACTAT	CTCTGGGCATCGCA	CAGTCTGCAACGGGAGACGGCTGGAGCG	2760
QY	2749	CGACTCTGTGCTCG	CCACCGCTACCGCT	CTCGGGATCGGTCAACCGTGCACATCCAAAC	2808
Db	2761	CGACTCTGTGCTCG	CCACCGCTACCGCT	CTCGGGATCGGTCAACCGTGCACATCCAAAC	2820
QY	2809	ATCAGAGGAGTGGCT	CTGTCCAGCACTGGA	AAATCCCTTTTATGGCAAGCCATCCCC	2868
Db	2821	ATCAGAGGAGTGGCT	CTGTCCAGCACTGGA	AAATCCCTTTTATGGCAAGCCATCCCC	2880
QY	2869	ATCAGAGCAATCA	AGGGGGGAGGACCT	CAATTTCTGCAATCCAGAGAAATGTGAT	2928
Db	2881	ATCAGAGCAATCA	AGGGGGGAGGACCT	CAATTTCTGCAATCCAGAGAAATGTGAT	2940
QY	2929	GAGCTCGCGCGAAG	CTATCGGCGCTCG	GACTCAATGTGTAGCAATTTACCGGGCCCTT	2988
Db	2941	GAGCTCGCGCGAAG	CTATCGGCGCTCG	GACTCAATGTGTAGCAATTTACCGGGCCCTT	3000
QY	2989	GATGTATCCGTAT	CAACCACTAGCGG	AGCGTCAATGTGTAGCAACGACGCTCTAATG	3048

Db	3001	GATGTATCCGTCATACCAACTAGCGAGAGCTTGTGTGTAGTAGCAGGAGCTTTAATG	3060
QY	3049	ACGGGCTTTACCGGCGATTTCACACTCAGTGATGCAGTGCAGTAATCATGTGTCAACCAGACA	3108
Dd	3061	ACGGGCTTTACCGGCGATTTCACACTCAGTGATGCAGTGCAGTAATCATGTGTCAACCAGACA	3120
QY	3109	GTGCACTTCAGCCTCGACCCGACCTTCACCATTTAGACAGCACCGTGCACAAAGACGGC	3168
Dd	3121	GTGCACTTCAGCCTCGACCCGACCTTCACCATTTAGACAGCACCGTGCACAAAGACGGC	3180
QY	3169	GTGTCA CGCTCGCAGCGCGAGGCAAGGACTGTGTAGGGGAGGATGGGCCATTTACAGTTTT	3228
Dd	3181	GTGTCA CGCTCGCAGCGCGAGGCAAGGACTGTGTAGGGGAGGATGGGCCATTTACAGTTTT	3240
QY	3229	GTGACTTCAGGAGAACGGCCCTCGGCGATGTTCGAATTCCTCGTTCTGTGCGAGTGCTAT	3288
Dd	3241	GTGACTTCAGGAGAACGGCCCTCGGCGATGTTCGAATTCCTCGTTCTGTGCGAGTGCTAT	3300
QY	3289	GACCGGGCTGTGTCTGTGTAGAGCTACGCGCCGCGAGACCTCAGTTAGTTGCGGGCT	3348
Dd	3301	GACCGGGCTGTGTCTGTGTAGAGCTACGCGCCGCGAGACCTCAGTTAGTTGCGGGCT	3360
QY	3349	TACCTAAACACACAGGGTTGCCGTGTGCAGGACCACTCTGGAGTTCTGGGAGAGCGTC	3408
Dd	3361	TACCTAAACACACAGGGTTGCCGTGTGCAGGACCACTCTGGAGTTCTGGGAGAGCGTC	3420
QY	3409	TTTACAGGCTTCACCCACATAGAGCCCATTTCTGTGCCAGACTAAGCAGGAGAGAC	3468
Dd	3421	TTTACAGGCTTCACCCACATAGAGCCCATTTCTGTGCCAGACTAAGCAGGAGAGAC	3480
QY	3469	AACCTCCCCTACCTGGTAGCATACACAGGCTACGGTGTGCGCGACGGCTCAGGCTCCACT	3528
Dd	3481	AACCTCCCCTACCTGGTAGCATACACAGGCTACGGTGTGCGCGACGGCTCAGGCTCCACT	3540
QY	3529	CCATCGTGGGACCAATGTGGAGTGTCTCATACGGCTAAGCCCTACGCTGCACGGGCA	3588
Dd	3541	CCATCGTGGGACCAATGTGGAGTGTCTCATACGGCTAAGCCCTACGCTGCACGGGCA	3600
QY	3589	ACGCCCTCTGTATAGGCTGGGAGCGGTTCAAACAGAGTTACTACACACCCCAT	3648
Dd	3601	ACGCCCTCTGTATAGGCTGGGAGCGGTTCAAACAGAGTTACTACACACCCCAT	3660
QY	3649	ACCAATACATATGCATGCATGTGCGGCTGACCTGGAGTGTCTGAGAGTGTGAGGCTG	3708
Dd	3661	ACCAATACATATGCATGCATGTGCGGCTGACCTGGAGTGTGAGAGTGTGAGGCTG	3720
QY	3709	CTGGTAGGCGGAGTCTTAGAGCTCTGGCGCGTATTTGCGTGACACAGGAGCGTGGTC	3768
Dd	3721	CTGGTAGGCGGAGTCTTAGAGCTCTGGCGCGTATTTGCGTGACACAGGAGCGTGGTC	3780
QY	3769	ATTGTGGGAGGATCATCTTTGTCGGAAGCGGCCATCATTTCCGACAGGAGTCCCT	3828
Dd	3781	ATTGTGGGAGGATCATCTTTGTCGGAAGCGGCCATCATTTCCGACAGGAGTCCCT	3840
QY	3829	TACCGGGAGTTTCGATGAGATGGAAGAGTGGCGCTCACACTCCCTTTACATCGAACAGGA	3888
Dd	3841	TACCGGGAGTTTCGATGAGATGGAAGAGTGGCGCTCACACTCCCTTTACATCGAACAGGA	3900
QY	3889	ATGCACTCGCGGACAAATTCAAAAGAAGGCAATCGGGTGTGTCGAAAACAGCCCAAG	3948
Dd	3901	ATGCACTCGCGGACAAATTCAAAAGAAGGCAATCGGGTGTGTCGAAAACAGCCCAAG	3960
QY	3949	CAAGCGGAGGCTGTCTCCCGTGTGGAATCCAAGTGGCGGACCTCGAAGCCTTCTGG	4008
Dd	3961	CAAGCGGAGGCTGTCTCCCGTGTGGAATCCAAGTGGCGGACCTCGAAGCCTTCTGG	4020
QY	4009	GCGAAGCATATGTGGAATTTTCATCAGCGGGATACAAATTTAGCAGGCTTTGCTCACTCG	4068
Dd	4021	GCGAAGCATATGTGGAATTTTCATCAGCGGGATACAAATTTAGCAGGCTTTGCTCACTCG	4080
QY	4069	CCTGGCAACCCCGGATAGCATCTGATGGCAATTCAGAGCTCTATCACAGCCCGCTC	4128

Db 4081 CCTGGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCTCTATCACAGCCGCGCTC 4140
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DB 7981 TGGCCTCTCTGCAGATCAAGT 8001

RESULT 5

US-09-539-601-28
; Sequence 28, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschlag, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct 1389/NS3-3'/19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS

/	LOCATION:	(1202)..(1812)
/	OTHER INFORMATION:	internal ribosome entry site from
/	OTHER INFORMATION:	encephalomyocarditis virus
/	FEATURE:	
/	NAME/KEY:	CDS
/	LOCATION:	(1813)..(7770)
/	OTHER INFORMATION:	hepatitis C virus nonstructural proteins NS3 - 5B
/	OTHER INFORMATION:	of cell culture adapted clone no. 19
/	FEATURE:	
/	NAME/KEY:	3'UTR
/	LOCATION:	(7771)..(8001)
/	US-09-539-601-28	
<hr/>		
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	Best Local Similarity	99.7%; Pred. No. 0;
	Matches 7973; Conservative	0; Mismatches 16; Indels 12; Gaps 1;
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Dd	61	TCTTTCACGCAGAAGCGTCTAGCCATGCGGTTAGTAGTGTCGTGCAGCCTCCAGGAC 120
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Dd	121	CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACGGGTAGTACACCGAATTGCCAG 180
Qy	181	GACGACCGGGTCTTTCTTGATCAAACCGCTCAATGCTCGAGATTGGGCGTGCCTCC 240
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Dd	241	GCAGACTCTAGCCGAGTAGTGTGGTTCGCGAAGCCCTTGTGTAATGCCTGATAGG 300
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Dd	301	GTGCTTGCAGTGCCTCCCGGAGGTCTCGTAGACCGTGACCATGAGCACGAATCCTAAC 360
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Dd	361	CTCAAGAAAAAACCAAACGTAACCAACGCGCGCCATGATTGAAACAAGATGGATTGC 420
Qy	409	ACGAGGTTCTCCGCGCGCTGGGTGGAGAGCTATTGGGTATGACTGGGCAACAAGA 468
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Dd	481	CAATCGGCTGCTCTGATGCGCGCTGTTCCGGCTGTACGCGCAGGGGCGCCGGTCTTT 540
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Qy	769	CGGCTACTCGCCATTTCGACCAACGAGAAAATCGCATCGAGCGAGCAGTACTCGGA 828
Dd	781	CGGCTACTCGCCATTTCGACCAACGAGAAAATCGCATCGAGCGAGCAGTACTCGGA 840

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DB	4141	ACCACCAACATACCTCTCTGTTTAAACATCTCGGGGAGATGGTGGCGCCCAACTTGGCT	4200	DB	5221	TGCGAGCCCGAAACCGGATGTAGCTGCTCACTTCCATGCTCAGCAGCCCTCCACATTT	5280
QY	4189	CCTCCAGCGCTGCTTCTGCTTTTCGTAGGAGCGGCGGATCGTGGAGCGGCTGTTGGCAGC	4248	QY	5269	ACGGCGGAGAGCGGTACGCTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCA	5328
DB	4201	CCTCCAGCGCTGCTTCTGCTTTTCGTAGGAGCGGCGGATCGTGGAGCGGCTGTTGGCAGC	4260	DB	5281	ACGGCGGAGAGCGGTACGCTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCA	5340
QY	4249	ATAGCGCTTGGGAGAGTCTGCTTGGATATTTTGGCAGGTTATGGAGCGGCTGGCAGGC	4308	QY	5329	TCAGCTACCGAGCTGCTGCGCTTCTTGTAGGCAACATGACCTACCGCTCATGACTCC	5388
DB	4261	ATAGCGCTTGGGAGAGTCTGCTTGGATATTTTGGCAGGTTATGGAGCGGCTGGCAGGC	4320	DB	5341	TCAGCTACCGAGCTGCTGCGCTTCTTGAAGCAACATGACCTACCGCTCATGACTCC	5400
QY	4309	GGCTCTGGTGGCTTTAAGTCAAGAGCGGAGATGCTCCACCGAGACCTGTTTAAAC	4368	QY	5389	CGGACGCTGACCTCATCGAGCCAACTCTCTGGCGGAGATCTCTGGAGGTTCCAGGAAATTC	5448
DB	4321	GGCTCTGGTGGCTTTAAGTCAAGAGCGGAGATGCTCCACCGAGACCTGTTTAAAC	4380	DB	5401	CGGACGCTGACCTCATCGAGCCAACTCTCTGGCGGAGATCTCTGGAGGTTCCAGGAAATTC	5460
QY	4369	CTACTCCCTGCTATCTCTCCCTGGCGCCCTAGTCTGGGCTGCTGGCGAGCGATA	4428	QY	5449	ACCCGCTGGAGTCAGAAATTAAGGTAGTAAATTTTGGACTCTTTGAGCGCTCCAAGCG	5508
DB	4381	CTACTCCCTGCTATCTCTCCCTGGCGCCCTAGTCTGGGCTGCTGGCGAGCGATA	4440	DB	5461	ACCCGCTGGAGTCAGAAATTAAGGTAGTAAATTTTGGACTCTTTGGAGCTCTTGGAGCGCTCCAAGCG	5520
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DB	4441	CTGCTGCGCAGCTGGGCGGAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCG	4500	DB	5521	GAGGAGGATGAGAGGAGGAGTATCCGTTCCGGCGGAGATCTCTGGGAGGTTCCAGGAAATTC	5580
QY	4489	TTGCTTTCGGGGTAAACAGCTCTCCCGACGACATATGTGCTGAGAGCGAGCTGCA	4548	QY	5569	CTCGAGCGATGCCCATATGGGCAAGCGGAGTAAACCCCTCACTGTTAGAGTCTCTGG	5628
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QY	4549	GCAGTGTCACTCAGATCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGCTTCAAC	4608	QY	5629	AGGACCCGAGTACCTCTCCCTCCAGTGTACACCGGTTGTCATTTGGCGCTGCCAAGGCC	5688
DB	4561	GCAGGATCACTCAGATCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGCTTCAAC	4620	DB	5641	AGGACCCGAGTACCTCTCCCTCCAGTGTACACCGGTTGTCATTTGGCGCTGCCAAGGCC	5700
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QY	4729	CGATTGCGGGGCTCCCTCTCTCATGTCAAGTGGGTACAGGGAGTCTGGCGGGC	4788	QY	5809	AGCGGACGCAACGGGCTCTCTGACAGCCCTCCGACGAGCGGCGGATCCGAC	5868
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DB	4921	ATTAAAGGATACACCGGCGCTTGACAGCCCTCCCGGCGCCAAATTTCTAGGGCG	4980	DB	6001	TCCTACACATGACAGCGGCTGATCAGCGCATGCGCTGCGGAGGAAACCAAGTGGCC	6060
QY	4969	CTGTGGCGGGTGGTGTGAGGAGTACGTGAGGTTACCGGGTGGGGATTTTCCACTAC	5028	QY	6049	ATCAATGACCTGAGCAACTCTTTGCTCGGTCAACAACTTGTGTCTATGCTACACATCT	6108
DB	4981	CTGTGGCGGGTGGTGTGAGGAGTACGTGAGGTTACCGGGTGGGGATTTTCCACTAC	5040	DB	6061	ATCAATGACCTGAGCAACTCTTTGCTCGGTCAACAACTTGTGTCTATGCTACACATCT	6120
QY	5029	GTGACGGCATGACCACTGACAAAGTAAAGTCCGCTGATGTTCCGGGCTCCGCGGCTTC	5088	QY	6109	CGGAGCGCAAGCTCGGCGAGAGGATGAGGAGTGTAGTGGAGCTCTCTGAGCGGAG	6168
DB	5041	GTGACGGCATGACCACTGACAAAGTAAAGTCCGCTGATGTTCCGGGCTCCGCGGCTTC	5100	DB	6121	CGGAGCGCAAGCTCGGCGAGAGGATGAGGAGTGTAGTGGAGCTCTCTGAGCGGAG	6180
QY	5089	TTTCAAGAGTGGATGGGCTGGTGGACAGTACGCTCCAGCGTGCAGAAACCCCTCTTA	5148	QY	6169	CACATACCGGAGCTCTCAAGGAGATGAAGCGGAGGCTCCACAGTGTAAAGGCTAAATTT	6228
DB	5101	TTTCAAGAGTGGATGGGCTGGTGGACAGTACGCTCCAGCGTGCAGAAACCCCTCTTA	5160	DB	6181	CACATACCGGAGCTCTCAAGGAGATGAAGCGGAGGCTCCACAGTGTAAAGGCTAAATTT	6240
QY	5149	CGGAGGAGGTCACTTCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCA	5208	QY	6229	CTATCCGTGGAGGAGCTGTAAAGTGAAGCTCCCGCCACATTCGGCGAGATCTAAATTTGGC	6288
DB	5161	CGGAGGAGGTCACTTCTGCTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCA	5220	DB	6241	CTATCCGTGGAGGAGCTGTAAAGTGAAGCTCCCGCCACATTCGGCGAGATCTAAATTTGGC	6300
				QY	6289	TAATGGGCAAGGAGCTCCGGAACCTTATCCAGCAAGGCGGTAAACACATCCGCTCCGTG	6348

Db	6301	TATGGGCNAAGGACGTCCGGAACCTATCCAGCAAGGCGGTAAACCACTCCGCTCCGGT	6360
QY	6349	TGGAAGGACTTGCTGGAAAGACACTGAGACACCAATTGACACCAACCATCATGGCGAAAAAT	6408
Db	6361	TGGAAGGACTTGCTGGAAAGACACTGAGACACCAATTGACACCAACCATCATGGCGAAAAAT	6420
QY	6409	GAGGTTTTCTGGGTCCAAACAGAGAGAGGGGGCGCAAGCGAGCTGCTTATCGTATTCT	6468
Db	6421	GAGGTTTTCTGGGTCCAAACAGAGAGAGGGGGCGCAAGCGAGCTGCTTATCGTATTCT	6480
QY	6469	CCAGATTTGGGGTTCTGGTGTGGAGAAATGCGCTTTACGATGTGGTCTCAACCTC	6528
Db	6481	CCAGATTTGGGGTTCTGGTGTGGAGAAATGCGCTTTACGATGTGGTCTCAACCTC	6540
QY	6529	CCTCAGCCGCTGATGGGCTCTTCATACGATTCCAACTACTCTCCTGAGACAGCGGTCGAG	6588
Db	6541	CCTCAGCCGCTGATGGGCTCTTCATACGATTCCAACTACTCTCCTGAGACAGCGGTCGAG	6600
QY	6589	TTCTCTGGTGAATGCTTGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGC	6648
Db	6601	TTCTCTGGTGAATGCTTGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGC	6660
QY	6649	TGTTTTGACTCAAACGCTCACTGAGAAATGACATCCGTTGAGAGTCAATCTACCAATGT	6708
Db	6661	TGTTTTGACTCAAACGCTCACTGAGAAATGACATCCGTTGAGAGTCAATCTACCAATGT	6720
QY	6709	TGTGACTTGGCCCCCGAAGCCAGACAGGCCATTAAGTTCGCTCACAGAGCGGCTTTACATC	6768
Db	6721	TGTGACTTGGCCCCCGAAGCCAGACAGGCCATTAAGTTCGCTCACAGAGCGGCTTTACATC	6780
QY	6769	GGGGGCCCCCTGACTAATTTCTAAGGCGCAAACTGCGGCTATCGCGGTCCCGCGAGC	6828
Db	6781	GGGGGCCCCCTGACTAATTTCTAAGGCGCAAACTGCGGCTATCGCGGTCCCGCGAGC	6840
QY	6829	GGTGTACTGACGACAGCTCGGTTAATACCTCACATGTATTCTTGAAGCGCGCTGGGCC	6888
Db	6841	GGTGTACTGACGACAGCTCGGTTAATACCTCACATGTATTCTTGAAGCGCGCTGGGCC	6900
QY	6889	TGTCGAGCTCGAAGCTTCCAGSAGTGCACGATCTCTGTATGCGGAGACGACCTTCTGTT	6948
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QY	6949	ATCTGTGAAGCGGGGACCCAAAGAGGACGAGCGAGCTTACGCGGCTTACCGAGGCT	7008
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Db	7021	ATGACTAGATACTCTGCCCCCTGCGGAGCCCGCCCAACCCAGAAATACGACTTGGAGTTG	7080
QY	7069	ATAACATCATGTCTCTCCATGTGTCAHGTGCGGACGATGCACTCTGGCAAAAGGCTGTAC	7128
Db	7081	ATAACATCATGTCTCTCCATGTGTCAHGTGCGGACGATGCACTCTGGCAAAAGGCTGTAC	7140
QY	7129	TATCTCACCCTGTACCCACCCCTTGGCGGGGTGCGTGGAGACAGCTAGACAC	7188
Db	7141	TATCTCACCCTGTACCCACCCCTTGGCGGGGTGCGTGGAGACAGCTAGACAC	7200
QY	7189	ACTCCAGTCAATTTCTGGCTTAGCAACATCATGTATGCGCCACCTTGTGGGCAAGG	7248
Db	7201	ACTCCAGTCAATTTCTGGCTTAGCAACATCATGTATGCGCCACCTTGTGGGCAAGG	7260
QY	7249	ATGATCCTGATGACTCATTTCTTCTCCATPCTTCTAGCTCAGGAACAACTTGAANAAGCC	7308
Db	7261	ATGATCCTGATGACTCATTTCTTCTCCATPCTTCTAGCTCAGGAACAACTTGAANAAGCC	7320
QY	7309	CTAGATTGTGAGATCTACGGGGCTGTCTACTCCATTGAGCCACTTGACCTACCTCAGATC	7368
Db	7321	CTAGATTGTGAGATCTACGGGGCTGTCTACTCCATTGAGCCACTTGACCTACCTCAGATC	7380
QY	7369	ATTCAACGACTCCATGGGCTTAGCGCATTTTCACCTTCCATAGTTACTCTCAGGTGAGATC	7428

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RESULT 6
US-09-539-601-4
; Sequence 4, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschlagler, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8637
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS2-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion
; OTHER INFORMATION: protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)

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OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1801)..(8406)
OTHER INFORMATION: hepatitis C virus NS2 - 5B
FEATURE:
NAME/KEY: 3' UTR
LOCATION: (8407)..(8637)
PUBLICATION INFORMATION:
AUTHORS: Lohmann, Volker
AUTHORS: Kner, Frank
AUTHORS: Koch, Jan-Oliver
AUTHORS: Herian, Ulrike
AUTHORS: Theilmann, Lorenz
AUTHORS: Bartenschlager, Ralf
TITLE: Replication of subgenomic hepatitis c virus RNAs in a
TITLE: hepatoma cell line
JOURNAL: Science
VOLUME: 285
PAGES: 110-113
DATE: 1999-07-02
US-09-539-601-4

Query Match 91.7%; Score 7331; DB 4; Length 8637;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 7989; Conservative 0; Mismatches 0; Indels 648; Gaps 1;
QY 1 GCCAGCCCCGATGGGGGCGACACCTCCACCATAGATCACTCCCTGTGTAGGAACACTACTG 60
DB 1 GCCAGCCCCGATGGGGGCGACACCTCCACCATAGATCACTCCCTGTGTAGGAACACTACTG 60
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DB 61 TCTTACGCGAAGCGCTAGCCATGGCGGTAGTATAGTGTGTCGACGCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGGACCATAGTGTCTCGGAAACCGGTAGTACACCGGAATTGCGAG 180
DB 121 CCCCCCTCCGGGAGGACCATAGTGTCTCGGAAACCGGTAGTACACCGGAATTGCGAG 180
QY 181 GACACCGGCTCTCTTCTTGATCAACCCGCTCAATCCCTGGAGATTGGCGGTGCCCC 240
DB 181 GACACCGGCTCTCTTCTTGATCAACCCGCTCAATCCCTGGAGATTGGCGGTGCCCC 240
QY 241 GCGAGACTGTAGCCGAGTAGTGTGGTTCGCGAAGCCCTTGTGCTACTGCTGATAGG 300
DB 241 GCGAGACTGTAGCCGAGTAGTGTGGTTCGCGAAGCCCTTGTGCTACTGCTGATAGG 300
QY 301 GTGCTTCGAGTGCCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTCGAGTGCCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
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DB 361 CTCAGAGAAACCAAGGGCGGCCATGATGTAACAAAGATGGAATTGCAACGAGTTCTC 420
QY 421 CGCGCGCTTGGGTGAGAGGCTATTCGCTATGCTGGCACACAGCAATCGCTGCT 480
DB 421 CGCGCGCTTGGGTGAGAGGCTATTCGCTATGCTGGCACACAGCAATCGCTGCT 480
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QY 541 ACCTGTCCGCTGCCCTGAATGAATGTCAGGACGAGCGCGGCTATGCTGGCTGGCA 600
DB 541 ACCTGTCCGCTGCCCTGAATGAATGTCAGGACGAGCGCGGCTATGCTGGCTGGCA 600
QY 601 CGACGGGCTTCTTGGCGAGCTGTGCTGAGTTGTCACTGAAGCGGAGGAGGACTGGC 660
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DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGCTACCTGCC 780
QY 781 CATTCGACCAACGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC 840
DB 781 CATTCGACCAACGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCGCAGCGGAACTGTCG 900
DB 841 TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCGCAGCGGAACTGTCG 900
QY 901 CCAGGCTCAAGGCGGCGATGCCCGAGCGGCGAGGATCTCGTGTGATCCCATGGCGCT 960
DB 901 CCAGGCTCAAGGCGGCGATGCCCGAGCGGCGAGGATCTCGTGTGATCCCATGGCGCT 960
QY 961 GCTTCCGGAATATCATGCTGGAATAATGGCGCTTCTCGATTCATCGACTGTGGCGGC 1020
DB 961 GCTTCCGGAATATCATGCTGGAATAATGGCGCTTCTCGATTCATCGACTGTGGCGGC 1020
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DB 1021 TGGGTGTGGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTCCTGAAGAGC 1080
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DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCTCCCTCCCTTAACGTTACTGGC 1260
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DB 1321 CCGTCTTTTGGCAATGAGGCGCGGAAACCTGCGCTCTCTCTTGTGAGGAGCATTCCT 1380
QY 1381 AGGGTCTTTCCTCTCGCAAGAGAAATGCAAGGATGCAAGGATGCTGTTGATGTCGTAAGAGCA 1440
DB 1381 AGGGTCTTTCCTCTCGCAAGAGAAATGCAAGGATGCAAGGATGCTGTTGATGTCGTAAGAGCA 1440
QY 1441 GTTCTCTTGAAGCTTCTTGAAGCAAAACAAACGCTGTAGGACCTTTTGAGCGAGCGG 1500
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DB 1501 AACCCCCCAGCTGTGCGACAGTGCCTCTGCGGCGCAAGCCACGCTGTATAGATACACT 1560
QY 1561 GCAAGGCGGCAACCCAGTGCACGCTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
DB 1561 GCAAGGCGGCAACCCAGTGCACGCTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
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DB 1681 ATGGATCTGATCTGGGCTCGCTGCGACATGCTTTACATGTTGTTAGTCCAGGTTAAAA 1740
QY 1741 AACGCTTAGGCCCCCGGAAACCAACGCGGAGCTGTTTCTCTTTGAAAAACAAGATATACC 1800

1741	Db	AACGCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTCTCAAAAAACACGATAATACC	1803
1801	Qy	ATG-----	1803
1801	Db	ATGACCGGAGATGGCAGCATCGTGGAGGGCGGTTTTCGTAGGTCGTACTACTTG	1860
1804	Qy	-----	1803
1861	Db	ACTTTGACCGCACTATAAGCTGTTCTTCGCTAGCTCATATGGTGTGTACAAATATTTT	1920
1804	Qy	-----	1803
1921	Db	ATCACCAGGGCGAGGCACATTGCAAGTGTGATCCCCCCTCAACGTCGGGGGGC	1980
1804	Qy	-----	1803
1981	Db	CGGATGCGTCATCCTCCTCAGGTGCGGATCCACCAGAGCTAATCTTTACCATCACC	2040
1804	Qy	-----	1803
2041	Db	AAAATCTGTCTGCCATACCTGGTCCACTCATGTGCTCCAGGCTGGTATATACCAAGTG	2100
1804	Qy	-----	1803
2101	Db	CCGTACTTGTGCGGGCACACGGGCTCATTCGTGCATGCTGTGGTGGAAAGTTGCT	2160
1804	Qy	-----	1803
2161	Db	GGGGTCATTATGTCAAATGGCTCTCATGAAGTTGGCGGCACTGACAGGTACGTACGTT	2220
1804	Qy	-----	1803
2221	Db	TATGACCATCTACCCACTGCGGGACTGGGCCACGGGCGCTACGAGACCTTGGCGTG	2280
1804	Qy	-----	1803
2281	Db	GCAGTTGAGCCCGTGTCTTCTCTGATATGAGACCAAGGTTATCATCTGGGGGCGAC	2340
1804	Qy	-----	1803
2341	Db	ACCGCGCGTGTGGGACATATCTTGGGCTGCCCGTCTCCGCGCAGGGGAGGGAG	2400
1804	Qy	-----GCGCTTATT	1812
2401	Db	ATACATCTGGACCGCAGACAGCTTGAAGGCAGGGTGGGACTCTCTCGGCTATT	2460
1813	Qy	ACGGCTACTTCCCAACAGACGGCAGCGCTACTTGGCTGCATATCATAGCCTCACAGGC	1872
2461	Db	ACGGCTACTTCCACAGACGGCAGCGCTACTTGGCTGCATCATCTAGCCTCACAGGC	2520
1873	Qy	CGGACAGAAACAGGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCAACACATCTTTC	1932
2521	Db	CGGCACAGAACAGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCAACACATCTTTC	2580
1933	Qy	CTGGGACTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCGGCTCAAGACC	1992
2581	Db	CTGGGACTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCGGCTCAAGACC	2640
1993	Qy	CTTGGCGGCCAAAGGGCCCAATCAACCAGGTCACACCAATGTGACACAGGACTCGTC	2052
2641	Db	CTTGGCGGCCAAAGGGCCCAATCAACCAGGTCACACCAATGTGACACAGGACTCGTC	2700
2053	Qy	GGTGGCAAGGCCCCCGGGCGGCTTCTTTGACACCATGACCTGCGGCGAGCTCGAC	2112
2701	Db	GGTGGCAAGGCCCCCGGGCGGCTTCTTTGACACCATGACCTGCGGCGAGCTCGAC	2760
2113	Qy	CTTTACTTGTTCACAGGATGCGGATGTATTCGGTGCCTGGCGGGCGACACGAGG	2172
2761	Db	CTTTACTTGTTCACAGGATGCGGATGTATTCGGTGCCTGGCGGGCGACACGAGG	2820
2173	Qy	GGGAGCCTACTCTCCCCCAGGCGGCTCTCTACTTTGAAGGCTCTTCGGGCGGTCCACTG	2232
2821	Db	GGGAGCCTACTCTCCCCCAGGCGGCTCTCTACTTTGAAGGCTCTTCGGGCGGTCCACTG	2880

QY	2233	CTCTGCCCTCGGGCACGCTGTGGGCATCTTTCCGGCTGCCGTGTGCACCCCGAGGGGTT	2292
DB	2881	CTCTGCCCTCGGGCACGCTGTGGGCATCTTTCCGGCTGCCGTGTGCACCCCGAGGGGTT	2940
QY	2293	CGGAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCGGTC	2352
DB	2941	CGGAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCGGTC	3000
QY	2353	TTCA CGGACAACTCGTCCCTCCGGCCGTACCGCAGACATTCCAGTGGCCCATCTACAC	2412
DB	3001	TTCA CGGACAACTCGTCCCTCCGGCCGTACCGCAGACATTCCAGTGGCCCATCTACAC	3060
QY	2413	GCCCTACTGTAGCGGCAAGACACTAAGGTGCCGCTCGGTATGTCAGCCCAAGGGTAT	2472
DB	3061	GCCCTACTGTAGCGGCAAGACACTAAGGTGCCGCTCGGTATGTCAGCCCAAGGGTAT	3120
QY	2473	AAGTGTCTTCCGAAACCGTCCGTCCCGCCACCCCTAGTTCCTGGGCGTATATGTCT	2532
DB	3121	AAGTGTCTTCCGAAACCGTCCGTCCCGCCACCCCTAGTTCCTGGGCGTATATGTCT	3180
QY	2533	AAGCACATGGTATCGGACCCTAA CATCAGAACCGGGTAAGGACCATCACACGGGTGCC	2592
DB	3181	AAGCACATGGTATCGGACCCTAA CATCAGAACCGGGTAAGGACCATCACACGGGTGCC	3240
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DB	3241	CCCATCAGTACTCCACTATGGCAAGTTCTTCGCCGACGTTGCTCTGGGGCGCC	3300
QY	2653	TATGACATCATATATGTGATGTCACCTCAACTGACTCGACCATATCTTGGGCATC	2712
DB	3301	TATGACATCATATATGTGATGTCACCTCAACTGACTCGACCATATCTTGGGCATC	3360
QY	2713	GGCACAGTCTCTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTGCTCGCACCGCT	2772
DB	3361	GGCACAGTCTCTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCTGCTCGCACCGCT	3420
QY	2773	AGCCTCCGGGATCGGTCA CCGTGCCACATCCAAACATCAGGAGGTGGCTCTGTCAGC	2832
DB	3421	AGCCTCCGGGATCGGTCA CCGTGCCACATCCAAACATCAGGAGGTGGCTCTGTCAGC	3480
QY	2833	ACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	2892
DB	3481	ACTGGAGAAATCCCTTTTATGGCAAAGCCATCCCATCGAGACCATCAAGGGGGGAGG	3540
QY	2893	CACCTCATTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCGGAAAGCTGTCGGC	2952
DB	3541	CACCTCATTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCGGAAAGCTGTCGGC	3600
QY	2953	CTCGACTCAATGCTGTAGCATATTACCGGGGCTTGATGTATCCCGTCATACCAACTAGC	3012
DB	3601	CTCGACTCAATGCTGTAGCATATTACCGGGGCTTGATGTATCCCGTCATACCAACTAGC	3660
QY	3013	GGAGACGTCAATGTCGTAGCAACGGA CGCTCTAATGACGGCTTTTACCGCGATTTCCGAC	3072
DB	3661	GGAGACGTCAATGTCGTAGCAACGGA CGCTCTAATGACGGCTTTTACCGCGATTTCCGAC	3720
QY	3073	TCAGTGATCGACTGCAATACATGCTGCTACCCAGACAGTGCATTAGCTGGACCCGACC	3132
DB	3721	TCAGTGATCGACTGCAATACATGCTGCTACCCAGACAGTGCATTAGCTGGACCCGACC	3780
QY	3133	TTACCAATTGAGACGACACCGTGCACAAGACGGGTGTCAAGTTCGAGCGGCGAGGC	3192
DB	3781	TTACCAATTGAGACGACACCGTGCACAAGACGGGTGTCAAGTTCGAGCGGCGAGGC	3840
QY	3193	AGGACTGTAGGGCAGGATGGGCATTTACAGTTTGTGACTCCAGGAAACGGCCCTCG	3252
DB	3841	AGGACTGTAGGGCAGGATGGGCATTTACAGTTTGTGACTCCAGGAAACGGCCCTCG	3900
QY	3253	GGCATGTTCCATTCCTCGGTTCTCTGCGAGTGCTATAGCGGGCTGTCTTGGTACGAG	3312
DB	3901	GGCATGTTCCATTCCTCGGTTCTCTGCGAGTGCTATAGCGGGCTGTCTTGGTACGAG	3960

QY	3313	CTACGCCCGCCGAGACCTCAGTTAGTTGGGCTTACCTAAACACACACACCGGTTGCC	3372	DB	5041	GGCGCCCTAGTCGTGGGGTCTGTGCGCAGGATACCTGCGTCGCGACGTTGGCGCCAGGG	5100
DB	3361	CTACGCCCGCCGAGACCTCAGTTAGTTGGGCTTACCTAAACACACACCGGTTGCC	4020	QY	4453	GAGGGGGTGTGCAGTGTGATGAACCGGTGTAGTTCGTTTCGGGGGTGAACACGCTC	4512
QY	3373	GTCTGCCAGGACCACTCTGGAGTTCTGGGAGAGCGTCTTTACAGGCGCTCACACATAGAC	3432	DB	5101	GAGGGGGTGTGCAGTGTGATGAACCGGTGTAGTTCGTTTCGGGGGTGAACACGCTC	5160
DB	4021	GTCTGCCAGGACCACTCTGGAGTTCTGGGAGAGCGTCTTTACAGGCGCTCACACATAGAC	4080	QY	4513	TCCCCACGCACTATGTGCTGAGAGCGACGCTGAGCAGCGTGTCACTCAGATCTCTCT	4572
QY	3433	GCCCATTTCTTGTCCAGACTAAGCAGGCGAGAGACAACTTCCCTTACCTGTGTAGCATAC	3492	DB	5161	TCCCCACGCACTATGTGCTGAGAGCGACGCTGAGCAGCGTGTCACTCAGATCTCTCT	5220
DB	4081	GCCCATTTCTTGTCCAGACTAAGCAGGCGAGAGACAACTTCCCTTACCTGTGTAGCATAC	4140	QY	4573	AGTCTTACCATCACTCAGCTGTGAAGGCTTTCACAGTGGATCAACAGAGACTGTCTCC	4632
QY	3493	CAGGCTACGCTGTGCGCCGAGGCTCAGGCTCAGGCTCCACCTCCATCTGTGGACCAAAATGTGAAG	3552	DB	5221	AGTCTTACCATCACTCAGCTGTGAAGGCTTTCACAGTGGATCAACAGAGACTGTCTCC	5280
DB	4141	CAGGCTACGCTGTGCGCCGAGGCTCAGGCTCAGGCTCCACCTCCATCTGTGGACCAAAATGTGAAG	4200	QY	4633	ACGCCATGTCCGGGCTCGTGGCTTAAGAGATGTTTGGGATTTGGATATGACGGTGTGACT	4692
QY	3553	TGTCTCATACGGCTAAAGCTACGCTGTCAAGGCGCAACGCCCTGTGTATAGGCTGGGA	3612	DB	5281	AGGCCATGTCCGGGCTCGTGGCTTAAGAGATGTTTGGGATTTGGATATGACGGTGTGACT	5340
DB	4201	TGTCTCATACGGCTAAAGCTACGCTGTCAAGGCGCAACGCCCTGTGTATAGGCTGGGA	4260	QY	4693	GATTTCAAGACCTCGGCTCCAGTCCCAAGCTTCCCGGAGTCCCGCTTCTTC	4752
QY	3613	GCGGTTCAAAACGAGGTTACTACACACACCCCATTAACCAATACATCATGGCATCATG	3672	DB	5341	GATTTCAAGACCTCGGCTCCAGTCCCAAGCTTCCCGGAGTCCCGCTTCTTC	5400
DB	4261	GCGGTTCAAAACGAGGTTACTACACACACCCCATTAACCAATACATCATGGCATCATG	4320	QY	4753	TCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATGCAAAACACCTGC	4812
QY	3673	TCGGCTGACCTGAGGTCGTCAAGGACCTGGGTGTGTAGGCGGAGTCTTAGCAGCT	3732	DB	5401	TCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATGCAAAACACCTGC	5460
DB	4321	TCGGCTGACCTGAGGTCGTCAAGGACCTGGGTGTGTAGGCGGAGTCTTAGCAGCT	4380	QY	4813	CCATGTGGAGCACAGATCAACCGACATGTGAATAAAGGTTCCATGAGGATCGTGGGCGCT	4872
QY	3733	CTGGCGGCTATTGCCCTGACAAACAGGACGCGTGTCTATTGTGGCGAGGATCATCTTGTC	3792	DB	5461	CCATGTGGAGCACAGATCAACCGACATGTGAATAAAGGTTCCATGAGGATCGTGGGCGCT	5520
DB	4381	CTGGCGGCTATTGCCCTGACAAACAGGACGCGTGTCTATTGTGGCGAGGATCATCTTGTC	4440	QY	4873	AGGACCTGTAGTAACAGCTGGCATGGAACATCCCGATTAACCGCTACACACGGGCGCCC	4932
QY	3793	GGAAAGCGCGCATCATCTCCGACAGGAAAGTCCCTTTACCGGAGTTCGATGAGATGAA	3852	DB	5521	AGGACCTGTAGTAACAGCTGGCATGGAACATCCCGATTAACCGCTACACACGGGCGCCC	5580
DB	4441	GGAAAGCGCGCATCATCTCCGACAGGAAAGTCCCTTTACCGGAGTTCGATGAGATGAA	4500	QY	4933	TGCACGCGCTCCCGCGCGCAAAATTTCTAGGCGCTGTGGCGGGTGGTGTGAGAG	4992
QY	3853	GAGTGGCGCTCACACCTCCCTTACATCAAGGAGGAAATGAGCTCGCGGAAACATTCAAA	3912	DB	5581	TGCACGCGCTCCCGCGCGCAAAATTTCTAGGCGCTGTGGCGGGTGGTGTGAGAG	5640
DB	4501	GAGTGGCGCTCACACCTCCCTTACATCAAGGAGGAAATGAGCTCGCGGAAACATTCAAA	4560	QY	4993	TACGTGGAGGTTACGCGGTTGGGGATTTCCATCTACGTGACGGGCGATGACCATGACAC	5052
QY	3913	CAGAAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGTGTGCTCCCGTG	3972	DB	5641	TACGTGGAGGTTACGCGGTTGGGGATTTCCATCTACGTGACGGGCGATGACCATGACAC	5700
DB	4561	CAGAAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGTGTGCTCCCGTG	4620	QY	5053	GTAAAGTCCCGTGTCAAGTTCGGCGCCCGGATTTCTTACAGAGTGGATGGGGTGGG	5112
QY	3973	GTGGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGGAGAGCATATGTGAAATTCATC	4032	DB	5701	GTAAAGTCCCGTGTCAAGTTCGGCGCCCGGATTTCTTACAGAGTGGATGGGGTGGG	5760
DB	4621	GTGGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGGAGAGCATATGTGAAATTCATC	4680	QY	5113	TTGCACAGGTACGCTCCAGCGTGAACCCCTCTTACGGGAGGAGTCAACATTCCTGTGC	5172
QY	4033	AGCGGATACAAATTTAGCAGGCTTGTCCACTGCTGCGCAACCCCGGATAGCATCA	4092	DB	5761	TTGCACAGGTACGCTCCAGCGTGAACCCCTCTTACGGGAGGAGTCAACATTCCTGTGC	5820
DB	4681	AGCGGATACAAATTTAGCAGGCTTGTCCACTGCTGCGCAACCCCGGATAGCATCA	4740	QY	5173	GGGCTCAATCAATACCTGGTTGGGTCAAGTCCCATGCGAGCCCGAACCGGACGTAGCA	5232
QY	4093	CTGATGGCATTCACAGCTCTATCACAGCCGCTCACACCCCAATACCTCTCTGTTT	4152	DB	5821	GGGCTCAATCAATACCTGGTTGGGTCAAGTCCCATGCGAGCCCGAACCGGACGTAGCA	5880
DB	4741	CTGATGGCATTCACAGCTCTATCACAGCCGCTCACACCCCAATACCTCTCTGTTT	4800	QY	5233	GTGCTCACTTCCATGCTCACGACCCCTCCCATATTACGGGAGACGGCTAAGCGTAGG	5292
QY	4153	AACATCTGGGGGATGGGTGGCGCCCACTTCTCCAGCGCTGCTTCTGCTTC	4212	DB	5881	GTGCTCACTTCCATGCTCACGACCCCTCCCATATTACGGGAGACGGCTAAGCGTAGG	5940
DB	4801	AACATCTGGGGGATGGGTGGCGCCCACTTCTCCAGCGCTGCTTCTGCTTC	4860	QY	5293	CTGGCCAGGGATCTCCCGCTTGTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	5352
QY	4213	GTAGGCGCGGATCGCTGGAGCGGCTGTGCGAGCATAGGCTTGGGAAGGTGTGTG	4272	DB	5941	CTGGCCAGGGATCTCCCGCTTGTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	6000
DB	4861	GTAGGCGCGGATCGCTGGAGCGGCTGTGCGAGCATAGGCTTGGGAAGGTGTGTG	4920	QY	5353	TCCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGACCTCATCGAGGCC	5412
QY	4273	GATATTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTGTGGCCCTTTAAGTCAIG	4332	DB	6001	TCCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGACCTCATCGAGGCC	6060
DB	4921	GATATTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTGTGGCCCTTTAAGTCAIG	4980	QY	5413	AACTCTCTGTGGCGGAGGATGGCGGGGAAATCACCCTGTGGAGTCAGAAAATAAG	5472
QY	4333	AGCGGCGAGATGCCCTCACCGAGGACCTGGTTAAGCTACTCCCTGCTACTCTCCCT	4392	DB	6061	AACTCTCTGTGGCGGAGGATGGCGGGGAAATCACCCTGTGGAGTCAGAAAATAAG	6120
DB	4981	AGCGGCGAGATGCCCTCACCGAGGACCTGGTTAAGCTACTCCCTGCTACTCTCCCT	5040	QY	5473	GTAGTAATTTGGACTCTTTTCGAGCGGCTCCAAAGCGGAGGATGAGAGGAGTATCC	5532
QY	4393	GGCGCCCTAGTCGTGGGGTCTGTGCGCAGCGATATGCTGCGGACGCTGGGCCAGGG	4452				

1009 ACTGTGCGCGCTGGGTGTCGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1068
1021 ACTGTGCGCGCTGGGTGTCGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1080
1069 TTGCTGAAGAGCTTGGCGGGAATGGGCTCAGCGCTTCTCGTGTCTTACGGTATCGCCG 1128
1081 TTGCTGAAGAGCTTGGCGGGAATGGGCTCAGCGCTTCTCGTGTCTTACGGTATCGCCG 1140
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1441 GTGAAGGAGCAGTTTCTCTGGAAGCTTCTTGAAGCAACCAACCTGCTGTAAGTGTG 1500
1489 TGCAGGAGCGGAACCCCGACCTGGGACAGGTGCTCTGGGCAAAAGCAGTGTGTA 1548
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1549 TAAGATACACCTGCAAGGCGGCAACCCCGACCTGGGACAGGTGCTCTGGGCAAAAGCAGTGTG 1608
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1609 GAAAGAGTCAAAATGGCTCTCTCAAGCTATTAACAGGCGGCTGGAAGTGTGTAAGTGTG 1668
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2221 GGTACGTAGCTTTATGACCATCTCACCCCACTCGGGGACTGGGCGCCACGCGGCGCTACGA 2280
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2281 GACCTTGGGTGCGAGTGTGAGCCCGTGTCTCTCTGATATGGAGACCAAGTTATCAACC 2340
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2221 GGCGGCTCACTGTCTCTCCCGTGGGCGGCTTCTTGGGCTCTTTCGCGCTGCGTGC 2280
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2521 GCGTATATGTCTAAGGACATGGTATCGACCTTAACATCAGAACCGGGGTGAAGGACCATC 2580

Db	3181	GCATATATGCTTAAGGACATGATGATGACACCTTAACATCAAGAACCGGGGTAAAGACCATC	3240
QY	2581	ACACGGGTGCCCCCATCAACGCTACTCACTATGCAAGAGTTTCTTGCCGACGGTGTGC	2640
Db	3241	ACACGGGTGCCCCCATCAACGCTACTCACTATGCAAGAGTTTCTTGCCGACGGTGTGC	3300
QY	2641	TCTGGGGGCGCTATGACATCAATAATATGTGATGAGTGCCTCACTGACTCGACCACT	2700
Db	3301	TCTGGGGGCGCTATGACATCAATAATATGTGATGAGTGCCTCACTGACTCGACCACT	3360
QY	2701	ATCTCTGGGATCGGCACAGCTCTGACCAAGCGGAGACGGCTGGAGCGACTCGTCTG	2760
Db	3361	ATCTCTGGGATCGGCACAGCTCTGACCAAGCGGAGACGGCTGGAGCGACTCGTCTG	3420
QY	2761	CTGCGCACCGCTACCGCTCGGGATCGGTCAACGAGGAGGAGGAGGAGGAGGAGG	2820
Db	3421	CTGCGCACCGCTACCGCTCGGGATCGGTCAACGAGGAGGAGGAGGAGGAGGAGG	3480
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC	2880
Db	3481	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC	3540
QY	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCACAGAGAAATGTGATGAGCTCGCGCG	2940
Db	3541	AAGGGGGGAGGACCTCATTTTCTGCCATTCACAGAGAAATGTGATGAGCTCGCGCG	3600
QY	2941	AAGCTGTCCGGCTCGGACCTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGTC	3000
Db	3601	AAGCTGTCCGGCTCGGACCTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGTC	3660
QY	3001	ATACCAACTAGCGAGACGTCATGTCTGACAAACGAGCGCTCTAATGACGGGTTTACC	3060
Db	3661	ATACCAACTAGCGAGACGTCATGTCTGACAAACGAGCGCTCTAATGACGGGTTTACC	3720
QY	3061	GGCGATTTGAGCTCAGTGATGACATCAATATGTGTACCCAGACAGTGCAGCTTCAGC	3120
Db	3721	GGCGATTTGAGCTCAGTGATGACATCAATATGTGTACCCAGACAGTGCAGCTTCAGC	3780
QY	3121	CTGAGCCGACCTTACCAATTTGAGACGACCGGTGCCAAGACGCGGTGTACGCTCG	3180
Db	3781	CTGAGCCGACCTTACCAATTTGAGACGACCGGTGCCAAGACGCGGTGTACGCTCG	3840
QY	3181	CAGCGCGGAGGACGACTGTTAGGGGAGGATGGGCATTTACAGTTTGTGACTCCAGGA	3240
Db	3841	CAGCGCGGAGGACGACTGTTAGGGGAGGATGGGCATTTACAGTTTGTGACTCCAGGA	3900
QY	3241	GAAACGGCTTGGGATGTTGATTTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGT	3300
Db	3901	GAAACGGCTTGGGATGTTGATTTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGT	3960
QY	3301	GCTTGTAGAGCTCAGCGCCCGGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA	3360
Db	3961	GCTTGTAGAGCTCAGCGCCCGGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA	4020
QY	3361	CCAGGGTTCGGCTGTGCGAGGACATCTGGAGTTCGGAGAGCTCTTACAGGCTTC	3420
Db	4021	CCAGGGTTCGGCTGTGCGAGGACATCTGGAGTTCGGAGAGCTCTTACAGGCTTC	4080
QY	3421	ACCCATAGACCCCATTTCTGTCAGACTTAAGCAGCAGGAGCAACTTCCCTTAC	3480
Db	4081	ACCCATAGACCCCATTTCTTGTCCAGACTTAAGCAGCAGGAGCAACTTCCCTTAC	4140
QY	3481	CTGGTAGACATACAGGCTACGGTGTGCGAGGCTCAGGCTCCACCTCCATCGTGGAC	3540
Db	4141	CTGGTAGACATACAGGCTACGGTGTGCGAGGCTCAGGCTCCACCTCCATCGTGGAC	4200
QY	3541	CAAAATGTGAGTGTCTCATACGGCTTAAGCTTACGCTGACGGGCAACGCGCTGCTG	3600
Db	4201	CAAAATGTGAGTGTCTCATACGGCTTAAGCTTACGCTGACGGGCAACGCGCTGCTG	4260
QY	3601	TATAGGCTGGAGCGGTTCAAAAGAGGTTTACTACCAACACACCCCAATAACATATC	3660
Db	4261	TATAGGCTGGAGCGGTTCAAAAGAGGTTTACTACCAACACACCCCAATAACATATC	4320
QY	3661	ATGATGATGATGCTGGGTCACCTGAGAGTCTGACGACCTGGTCTGCTAGGCGGA	3720
Db	4321	ATGATGATGATGCTGGGTCACCTGAGAGTCTGACGACCTGGTCTGCTAGGCGGA	4380
QY	3721	GTCTTAGAGCTCTGGGCGGCTATGCTGACAAACAGGAGCGTGTCTATTTGGGCGAG	3780
Db	4381	GTCTTAGAGCTCTGGGCGGCTATGCTGACAAACAGGAGCGTGTCTATTTGGGCGAG	4440
QY	3781	ATCATCTTGTTCGGAAGCCGCTCATTTCCCGACAGGAAAGTCTTTTACCGGAGTTC	3840
Db	4441	ATCATCTTGTTCGGAAGCCGCTCATTTCCCGACAGGAAAGTCTTTTACCGGAGTTC	4500
QY	3841	GATGATGATGAAAGTGGGCTCTCACCTCCCTTACATCGAAGGAAATGAGCTCGCC	3900
Db	4501	GATGATGATGAAAGTGGGCTCTCACCTCCCTTACATCGAAGGAAATGAGCTCGCC	4560
QY	3901	GAAACATTTCAAAACAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCAAGCGGAGCT	3960
Db	4561	GAAACATTTCAAAACAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCAAGCGGAGCT	4620
QY	3961	GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATG	4020
Db	4621	GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATG	4680
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Db	4681	TGGAATTTTCAATCAGCGGATACAAATATTTAGAGAGCTTCTCACTCTGCTGCAACCCC	4740
QY	4081	GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4140
Db	4741	GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4800
QY	4141	ACCTCTCTGTTTAACTCTGGGGGATGGTGGCGCCGCAACTTGTCTCTCCAGCGCT	4200
Db	4801	ACCTCTCTGTTTAACTCTGGGGGATGGTGGCGCCGCAACTTGTCTCTCCAGCGCT	4860
QY	4201	GCTTCTGCTTTCGAGGCGCGGATCGTGGAGGCTGTGGCAGCATAGGCTTGGG	4260
Db	4861	GCTTCTGCTTTCGAGGCGCGGATCGTGGAGGCTGTGGCAGCATAGGCTTGGG	4920
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Db	4921	AAGTGTCTGTTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCTCTGTCGC	4980
QY	4321	TTTAAAGTCTATGAGCGGAGATGCTTCCACCGAGGACCTGGTTAACTTCTCTCTGCT	5040
Db	4981	TTTAAAGTCTATGAGCGGAGATGCTTCCACCGAGGACCTGGTTAACTTCTCTCTGCT	5040
QY	4381	ATCTCTCTCCCTGGCGGCTAGTCTGGGGTCTGTCGAGGATGATGCTGCTGGGAC	4440
Db	5041	ATCTCTCTCCCTGGCGGCTAGTCTGGGGTCTGTCGAGGATGATGCTGCTGGGAC	5100
QY	4441	GTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	4500
Db	5101	GTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5160
QY	4501	GTTAAACGAGTCTTCCCGGACGCTATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGG	4560
Db	5161	GTTAAACGAGTCTTCCCGGACGCTATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGG	5220
QY	4561	CAGATCTCTCTAGTCTTACCATCTAGCTGCTGAGAGGCTTCCAGTGGATCAAC	4620
Db	5221	CAGATCTCTCTAGTCTTACCATCTAGCTGCTGAGAGGCTTCCAGTGGATCAAC	5280
QY	4621	GAGGAGTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	4680
Db	5281	GAGGAGTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5340
QY	4681	ACGGTGTGATGATTTCAAGACCTGGCTCCAGTCCAGGCTCTGCGGAGTTCGGGGA	4740
Db	5341	ACGGTGTGATGATTTCAAGACCTGGCTCCAGTCCAGGCTCTGCGGAGTTCGGGGA	5400

Db 7561 AAGCTCCAGGACTGACAGTCTGCTATGCGGAGACGACCTTGCTGTTATCTGTGAAGC 7620
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Db 7621 GCGGGGACCCAGAGCAGAGCGAGCGCTACGGGCTTTCACGAGGCTATGACTAGATAC 7680
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Qy 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
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Qy 7981 AGATCAAGT 7989

Db 8641 AGATCAAGT 8649
RESULT 8
US-10-029-907-1
; Sequence 1, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8639
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1803)...(8408)
US-10-029-907-1
Query Match 91.0%; Score 7273.8; DB 4; Length 8639;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 7976; Conservative 0; Mismatches 2; Indels 671; Gaps 3;
Qy 1 GCCAGCCCCGATGGGGGCGACATCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60
Db 2 GCCAGCCCCGATGGGGGCGACATCCACCATAGATCACTCCCTGTGAGGAAGTACTG 61
Qy 61 TCTTACGCGAAGAGCTCTAGCATGGCGTTAGTATGAGTGTGTCGAGCCTCCAGAC 120
Db 62 TCTTACGCGAAGAGCTCTAGCATGGCGTTAGTATGAGTGTGTCGAGCCTCCAGAC 121
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Qy 241 GCGAGACTGTAGCCGAGTGTGGTCCGAAAGGCTTGTGCTACTGCTGATAGG 300
Db 242 GCGAGACTGTAGCCGAGTGTGGTCCGAAAGGCTTGTGCTACTGCTGATAGG 301
Qy 301 GTGCTTGGAGTGTCCCGGAGGTCTCGTAGCCGTGACCATGAGCAGATCCTAAAC 360
Db 302 GTGCTTGGAGTGTCCCGGAGGTCTCGTAGCCGTGACCATGAGCAGATCCTAAAC 361
Qy 361 CTCAGAGAAACCAAGAGGCGCGCATGATGAACAGATGATTTGACGAGGTTCTC 420
Db 362 CTCAGAGAAACCAAGAGGCGCGCATGATGAACAGATGATTTGACGAGGTTCTC 421
Qy 421 CGCGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGT 480
Db 422 CGCGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGT 481
Qy 481 CTGATGCGCGCTGTTCGGCTGTGAGCGGGGCGCGGTTCTTTTGTCAAGACCG 540
Db 482 CTGATGCGCGCTGTTCGGCTGTGAGCGGGGCGCGGTTCTTTTGTCAAGACCG 541
Qy 541 ACTGTCCGCTGCTGATGAGTCAAGAGGAGGAGCGGCTATCGTGGTGGCCA 600
Db 542 ACTGTCCGCTGCTGATGAGTCAAGAGGAGGAGGAGGCTATCGTGGTGGCCA 601
Qy 601 CGAGCGGCGTTCCTTCCGCGAGTGTCTCGAGTGTCTCACTGAAGCGGAGGAGTGGC 660

Db	602	CGACGGGGTTCCTTGGCAGCTGTGCTCGACGTTGTCTACATGAAGGGGAAAGGAGCTGGC	661
Qy	661	TGCTATTGGGCGAAGTCCGGGGCAGAGATCTCTGTCTCATCTCACTTGTCTCTCTCCGCGAGA	720
Db	662	TGCTATTGGGCGAAGTCCGGGGCAGAGATCTCTGTCTCATCTCACTTGTCTCTCTCCGCGAGA	721
Qy	721	AAGTATCCATCATGGCTGATGCAATCGGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780
Db	722	AAGTATCCATCATGGCTGATGCAATCGGCGGCTGCATACGCTTGATCCGGCTACCTGCC	781
Qy	781	CATTGCAACCAAGCGAAACATCGCATCGAGCGAGCAGCTACTCTCGATGGAAGCGGTC	840
Db	782	CATTGCAACCAAGCGAAACATCGCATCGAGCGAGCAGCTACTCTCGATGGAAGCGGTC	841
Qy	841	TTGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGGCCAGCGAACTGTTGC	900
Db	842	TTGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGGCCAGCGAACTGTTGC	901
Qy	901	CCAGGCTCAAGGCGCGATGCGCGAGCGAGGATCTCTGTCGTGACCCATGGCGATGCC	960
Db	902	CCAGGCTCAAGGCGCGATGCGCGAGCGAGGATCTCTGTCGTGACCCATGGCGATGCC	961
Qy	961	GCTTGGCGAATATCATGGTGGAAATGGCGCTTTCTGATTCATCGACTGTGGCGGC	1020
Db	962	GCTTGGCGAATATCATGGTGGAAATGGCGCTTTCTGATTCATCGACTGTGGCGGC	1021
Qy	1021	TGGGTCGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAC	1080
Db	1022	TGGGTCGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAC	1081
Qy	1081	TTGGCGGGAATGGGCTGACCGCTTCTCTGCTCTTACGGTATCGCGCTCCGATTCGC	1140
Db	1082	TTGGCGGGAATGGGCTGACCGCTTCTCTGCTCTTACGGTATCGCGCTCCGATTCGC	1141
Qy	1141	AGCGCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAA	1188
Db	1142	AGCGCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAA	1201
Qy	1189	CAGACCAACAGGTTTCCCTCTAGCGGATCATATTCGCGCCCTCTCCCTCCCGCCCGCT	1248
Db	1202	CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT	1250
Qy	1249	AACGTTACTGGCGGAAGCGCTTGAATAAGCGGTGTGTGTCTATGTTATTT	1308
Db	1251	AACGTTACTGGCGGAAGCGCTTGAATAAGCGGTGTGTGTCTATGTTATTT	1310
Qy	1309	TCACCATATTGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTCTTG	1368
Db	1311	TCACCATATTGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTCTTG	1370
Qy	1369	ACGAGCATTCCTAGGGCTCTTCCCTCTGCGCAAGGATGCAAGGTTCTGTTGAATGTC	1428
Db	1371	ACGAGCATTCCTAGGGCTCTTCCCTCTGCGCAAGGATGCAAGGTTCTGTTGAATGTC	1430
Qy	1429	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGGACCCCT	1488
Db	1431	GTGAAGGAGCAGTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGGACCCCT	1490
Qy	1489	TGCAAGGAGGGAACCCCTCTGCGGACAGGTCCTCTGCGGCAAGGATGCAAGGTTCTG	1548
Db	1491	TGCAAGGAGGGAACCCCTCTGCGGACAGGTCCTCTGCGGCAAGGATGCAAGGTTCTG	1550
Qy	1549	TAAGATACCTCTCAAGGCGGACAAACCCAGTGCCACCTGTGAGTTGGATGTTG	1608
Db	1551	TAAGATACCTCTCAAGGCGGACAAACCCAGTGCCACCTGTGAGTTGGATGTTG	1610
Qy	1609	GAAAGAGTCAATGGCTCTCTCAAGGATTTCAACAAAGGGCTGAAGGATGCCAGAAG	1668
Db	1611	GAAAGAGTCAATGGCTCTCTCAAGGATTTCAACAAAGGGCTGAAGGATGCCAGAAG	1670
Qy	1669	GTACCCCATTTGATGGATCTGATCTGGGCGCTCGGTGACATGCTTTACATGTTTAG	1728
Db	1671	GTACCCCATTTGATGGATCTGATCTGGGCGCTCGGTGACATGCTTTACATGTTTAG	1730
Qy	1729	TCGAGGTTAAAAACGTTAGGCCCCCCCCGAAACCAAGGGGAGCTGTTTCTTTGAAAAA	1788
Db	1731	TCGAGGTTAAAAACGTTAGGCCCCCCCCGAAACCAAGGGGAGCTGTTTCTTTGAAAAA	1790
Qy	1789	CACGATAATACCATG-----	1803
Db	1791	CACGATAATACCATGAGACCGGAGATGCGAGCATCTGTCGGAGGCGGTTTCTGTTAGT	1850
Qy	1804	-----	1803
Db	1851	CTGATACCTCTTGACCTTGTCACCGCATATAAGCTGTTCCTCGCTAGGCTCATATGTTG	1910
Qy	1804	-----	1803
Db	1911	TTACAAATTTTATCACCAGGGCGGAGGACACTTGCAGTGTGGATCCCGCCCTCAAC	1970
Qy	1804	-----	1803
Db	1971	GTTGGGGGGGCGCGATGCGCTCATCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	2030
Qy	1804	-----	1803
Db	2031	TTTACCATCACCAGGCTTGTCTCGCCATCTCGGTCCACTCATGTTGTTCCAGGCTGGT	2090
Qy	1804	-----	1803
Db	2091	ATAACAAAGTCCGCTTCTGTCGGCGCACACGGGCTCATCTCGTGCATGCTGTTG	2150
Qy	1804	-----	1803
Db	2151	CGGAAGTTGCTGGGGTCAATTATGTCCAATTTGCTCTCATGAAAGTTGGCGCACGTGACA	2210
Qy	1804	-----	1803
Db	2211	GCTACGTAGCTTTATGACCATCTCACCCACTGCGGGACTGGGCGGCGGCGCTACGA	2270
Qy	1804	-----	1803
Db	2271	GACCTTGGCTGGAGTTGAGCCCGTCTCTCTCTCTGATATGAGACCAAGGTTATCACC	2330
Qy	1804	-----	1803
Db	2331	TGGGGGCGAGACCCGCGCGTGTGGGACATCATCTTGGGCTTCCCGCTCTCCGCGCGC	2390
Qy	1804	-----	1803
Db	2391	AGGGGAGGAGATACATCTGGGACCGGACAGCCCTTGAAGGGGAGGGGTGGCGACTC	2450
Qy	1804	-----	1803
Db	2451	CTCGCGCTTATAGCGCTTACTCCAAACAGACGCGAGGCTCTTGGCTGCATCATCACT	2510
Qy	1861	AGCTTCACAGCGCGGACAGGACAGGTCAGGGGAGGTCGAAAGTGTCTCCACGCA	1920
Db	2511	AGCTTCACAGCGCGGACAGGACAGGTCAGGGGAGGTCGAAAGTGTCTCCACGCA	2570
Qy	1921	ACAAATCTTCTTCTGCGCTCTGCTCAATGGCGTGTGTGGACTGTCTCATATGTTGCC	1980
Db	2571	ACAAATCTTCTTCTGCGCTCTGCTCAATGGCGTGTGTGGACTGTCTCATATGTTGCC	2630
Qy	1981	GGCTCAAGACCTTCTCGCGCCCAAGGGCCCAATCAACCCAAATGTACACCAATGTGGAC	2040
Db	2631	GGCTCAAGACCTTCTCGCGCCCAAGGGCCCAATCAACCCAAATGTACACCAATGTGGAC	2090
Qy	2041	CAGGACCTCTGCTGGCTGGCAAGGCGGCGGCGGCGGCTTCTTGAACCATGCACTGC	2100
Db	2691	CAGGACCTCTGCTGGCTGGCAAGGCGGCGGCGGCGGCTTCTTGAACCATGCACTGC	2750
Qy	2101	GGCAGCTCGGACCTTCTTCTGCTGCGGCGGCGGCGGCGGCTTCTTGAACCATGCACTGC	2160
Db	2751	GGCAGCTCGGACCTTCTTCTGCTGCGGCGGCGGCGGCGGCTTCTTGAACCATGCACTGC	2810

Qy	2161	GGCGACAGAGGGGAGGCTACTCTCCCGCAGGCGCGTCTCTACTTGAAGGCTCTTCG	2220	3891	GAACGGCCCTCGGGGANTGTTGATTCCTCGGTTCTGTGCGAGTGTATGAACGGCGGCTGT	3950
Db	2811	GGCGACAGAGGGGAGGCTACTCTCCCGCAGGCGCGTCTCTACTTGAAGGCTCTTCG	2870	3301	GCTTGGTACGAGCTCAAGCCCGCCGAGACCTCAGTTAGGTTCCGGGCTTACCTAACACA	3360
Qy	2221	GGCGGTCACTGCTCTGCCCTCGGGGACGCTGTGGGCTCTTTCGGGCTCCCGTGTGC	2280	3951	GCTTGGTACGAGCTCAAGCCCGCCGAGACCTCAGTTAGGTTCCGGGCTTACCTAACACA	4010
Db	2871	GGCGGTCACTGCTCTGCCCTCGGGGACGCTGTGGGCTCTTTCGGGCTCCCGTGTGC	2930	3361	CCAGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTTGGAGAGCGCTCTTACAGGCTTC	3420
Qy	2281	ACCCGAGGGTTCGGAAGCGGTGGACTTTGTACCCGTCAGGCTATGGAACCACTATG	2340	4011	CCAGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTTGGAGAGCGCTCTTACAGGCTTC	4070
Db	2931	ACCCGAGGGTTCGGAAGCGGTGGACTTTGTACCCGTCAGGCTATGGAACCACTATG	2990	3421	ACCCATAGAGCGCCATTTCTTGTCCAGACTTAAGCAGCGAGGAGACAACTTCCCTTAC	3480
Qy	2341	CGGTCCCGGCTCTTACGAGCAAACTCGTCCCTCCGCGGTACCGCAGACATTCAGGTTG	2400	4071	ACCCATAGAGCGCCATTTCTTGTCCAGACTTAAGCAGCGAGGAGACAACTTCCCTTAC	4130
Db	2991	CGGTCCCGGCTCTTACGAGCAAACTCGTCCCTCCGCGGTACCGCAGACATTCAGGTTG	3050	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCAGCTCCATCTCCATCGTGGAC	3540
Qy	2401	GCCATCTACAGCCCTCTAGGTAGCGGCAAGAGCACTAAGGTGCGGCTCGGTATGCA	2460	4131	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCAGCTCCATCTCCATCGTGGAC	4190
Db	3051	GCCATCTACAGCCCTCTAGGTAGCGGCAAGAGCACTAAGGTGCGGCTCGGTATGCA	3110	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCTTACGCTGACGCGGCAACGCGCTCTCTG	3600
Qy	2461	GCCCAAGGGTATAAGGTGCTTGTCTGAACCCGTCGTCGCGGCAACCTAGGTTTCGG	2520	4191	CAAAATGTGAAGTGTCTCATACGGCTAAAGCTTACGCTGACGCGGCAACGCGCTCTCTG	4250
Db	3111	GCCCAAGGGTATAAGGTGCTTGTCTGAACCCGTCGTCGCGGCAACCTAGGTTTCGG	3170	3601	TATAGCTGGAGCGCTTCAAAAACGAGGTTACTACCAACACACCCCATTAACAAATACATC	3660
Qy	2521	GCGTATATGTCTAAGGACATGTTATCGACCTTAACATCAGAACCGGGGTAAAGACCATC	2580	4251	TATAGCTGGAGCGCTTCAAAAACGAGGTTACTACCAACACACCCCATTAACAAATACATC	4310
Db	3171	GCGTATATGTCTAAGGACATGTTATCGACCTTAACATCAGAACCGGGGTAAAGACCATC	3230	3661	ATGSCATGCTATGTCGGCTGACCTTGGAGTGTCTACAGGACCTGGTGTGGTAGGCGGA	3720
Qy	2581	ACCAAGGGTCCCGCTACGCTACTTCCACCTATGCGCAAGTTTCTTGGCGAGCGTGTGC	2640	4311	ATGSCATGCTATGTCGGCTGACCTTGGAGTGTCTACAGGACCTGGTGTGGTAGGCGGA	4370
Db	3231	ACCAAGGGTCCCGCTACGCTACTTCCACCTATGCGCAAGTTTCTTGGCGAGCGTGTGC	3290	3721	GTCTAGAGCTTGGCGGCTATGCTGACACAGCAGCGCTGCTCATTTGTGGGACG	3780
Qy	2641	TCTGGGCGGCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTGACCACT	2700	4371	GTCTAGAGCTTGGCGGCTATGCTGACACAGCAGCGCTGCTCATTTGTGGGACG	4430
Db	3291	TCTGGGCGGCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTGACCACT	3350	3781	ATCATCTGTCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCTTTACCGGAGTTC	3840
Qy	2701	ATCTGGGCTACGACAGTCTGACCAAGGAGAGCGGTGGAGCGGCTCTGCTGT	2760	4431	ATCATCTGTCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCTTTACCGGAGTTC	4490
Db	3351	ATCTGGGCTACGACAGTCTGACCAAGGAGAGCGGTGGAGCGGCTCTGCTGT	3410	3841	GATGAGTGGAGAGTGGCGCTCAACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC	3900
Qy	2761	CTCGCCAGGCTACGCTCGGGTACGCTGCGGACGCTGCGGAGCGGCTGCTGCTGT	3470	4491	GATGAGTGGAGAGTGGCGCTCAACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC	4550
Db	3411	CTCGCCAGGCTACGCTCGGGTACGCTGCGGACGCTGCGGAGCGGCTGCTGCTGT	3470	3901	GAACTTCAACACAGAGGCTATCGGTTGCTGCAACAGCCACCAAGCAAGCGGAGGCT	3960
Qy	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCAATCGAGACCATC	2880	4551	GAACTTCAACACAGAGGCTATCGGTTGCTGCAACAGCCACCAAGCAAGCGGAGGCT	4610
Db	3471	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCAATCGAGACCATC	3530	3961	GCTGCTCCGCTGCTGCAATCCAAAGTGGGCGGACCTCTCGAAGCCTTTCTGGGCGAAGCATATG	4020
Qy	2881	AAGGGGGGAGGGA CTTCTATTTCTGCTCAATCCAGAGAAATGTGATGAGCTCGCGCG	2940	4611	GCTGCTCCGCTGCTGCAATCCAAAGTGGGCGGACCTCTCGAAGCCTTTCTGGGCGAAGCATATG	4670
Db	3531	AAGGGGGGAGGGA CTTCTATTTCTGCTCAATCCAGAGAAATGTGATGAGCTCGCGCG	3590	4021	TGGAAATTTTCATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCC	4080
Qy	2941	AAGCTGTCGGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTATGATGATCCGTC	3000	4671	TGGAAATTTTCATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCC	4730
Db	3591	AAGCTGTCGGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTATGATGATCCGTC	3650	4081	GCGATAGATCACTGATGCACTTACAGGCTTATCCACAGCGCGCTTACCAACCAACAT	4140
Qy	3001	ATACCAACTAGCGGAGAGCTGATTTGTGTAAGCAAGCAAGCTCTATGAGCGGCTTACC	3060	4731	GCGATAGATCACTGATGCACTTACAGGCTTATCCACAGCGCGCTTACCAACCAACAT	4790
Db	3651	ATACCAACTAGCGGAGAGCTGATTTGTGTAAGCAAGCAAGCTCTATGAGCGGCTTACC	3710	4141	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGGCGCAACTTGTCTCTCCAGGCT	4200
Qy	3061	GGCGATTTGCACTCAGTATGCACTGCAATACATGTTGTCACCCAGACAGTTCGACTTCAGC	3120	4791	ACCTCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGGCGCAACTTGTCTCTCCAGGCT	4850
Db	3711	GGCGATTTGCACTCAGTATGCACTGCAATACATGTTGTCACCCAGACAGTTCGACTTCAGC	3770	4201	GCTTCTGCTTTTCTAGCGCGGCTATGCGAGCGGCTTGTGGAGCATAGAGCTTGGG	4260
Qy	3121	CTGACCCGACCTTCAACATTTAGACAGCAGCGGTGCGCAACAGCGGCTGTCAGCTCG	3180	4851	GCTTCTGCTTTCTAGCGCGGCTATGCGAGCGGCTTGTGGAGCATAGAGCTTGGG	4910
Db	3771	CTGACCCGACCTTCAACATTTAGACAGCAGCGGTGCGCAACAGCGGCTGTCAGCTCG	3830	4261	AAGTGTCTGTTGATATTTTGGCAGGTTATGCGAGCGGCTGGCAGCGCGCTCTGCGCC	4320
Qy	3181	CAGCGGAGGACAGGACTGTGTAGGGGCGAGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240	4911	AAGTGTCTGTTGATATTTTGGCAGGTTATGCGAGCGGCTGGCAGCGCGCTCTGCGCC	4970
Db	3831	CAGCGGAGGACAGGACTGTGTAGGGGCGAGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3890	4321	TTTAAAGTCAATGAGCGGCGAGATGCCCTCAACCGAGGACCTGTTTAACTACTTCCCTGCT	4380
Qy	3241	GAACGGCCCTCGGGCACTGTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGCTGT	3300			

Db 242 CGAGCTGTAGCCGAGTAGTGTGGTTCGGAAAGGCCCTTGTGGTACTGCTGTATAGG 301
QY 302 TGCTTGGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAACC 361
Db 302 TGCTTGGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAACC 361
QY 362 TCAAGAAAAACAAMAGGCGCCCATGATTAACAAAGATGGATTGCAACGAGTTCTCC 421
Db 362 TCAAGAAAAACAAMAGGCGCCCATGATTAACAAAGATGGATTGCAACGAGTTCTCC 421
QY 422 GCGCGTTGGTGGAGAGCTATTCCGCTATGACTGGGCAACAGACATCCGCTGCTC 481
Db 422 GCGCGTTGGTGGAGAGCTATTCCGCTATGACTGGGCAACAGACATCCGCTGCTC 481
QY 482 TGATGCGCGCTGTTCCGGTGTGAGCGCAGGGCGCCCGGTTCTTTTGTCAAGACCGA 541
Db 482 TGATGCGCGCTGTTCCGGTGTGAGCGCAGGGCGCCCGGTTCTTTTGTCAAGACCGA 541
QY 542 CCTGTCCGGTGCCTCAATGAATGACGACGAGCAGGCGGGCTATCGTGGCTGCCAC 601
Db 542 CCTGTCCGGTGCCTCAATGAATGACGACGAGCAGGCGGGCTATCGTGGCTGCCAC 601
QY 602 GACGGCGTTCTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGCTGGCT 661
Db 602 GACGGCGTTCTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGCTGGCT 661
QY 662 GCTATTGGCGAAGTGCCTGGCGAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAA 721
Db 662 GCTATTGGCGAAGTGCCTGGCGAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAA 721
QY 722 AGTATCCATCATGCTGATGCAATGCGGCGGTGATAGCTTGTATCGGCTACCTGCC 781
Db 722 AGTATCCATCATGCTGATGCAATGCGGCGGTGATAGCTTGTATCGGCTACCTGCC 781
QY 782 ATTGCACCAAGCAAGCAATCGCATCGAGCAGCATCTCGATGGAAGCGCGTCT 841
Db 782 ATTGCACCAAGCAAGCAATCGCATCGAGCAGCATCTCGATGGAAGCGCGTCT 841
QY 842 TGTGATCAGATGATCTGACGAGAGCATCAGGGGCTCGCGGCGAGCACTGTTCCG 901
Db 842 TGTGATCAGATGATCTGACGAGAGCATCAGGGGCTCGCGGCGAGCACTGTTCCG 901
QY 902 CAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCGTGTGACCCATGCGGATGCTG 961
Db 902 CAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCGTGTGACCCATGCGGATGCTG 961
QY 962 CTTGCCGAATATCATGTTGGAATGCGCGTCTTCTGGATTGATCGACTGTGCGCGCT 1021
Db 962 CTTGCCGAATATCATGTTGGAATGCGCGTCTTCTGGATTGATCGACTGTGCGCGCT 1021
QY 1022 GGGTGTGGCGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATTTGCTGAAGACT 1081
Db 1022 GGGTGTGGCGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATTTGCTGAAGACT 1081
QY 1082 TGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTACGCTATCGCGCTCCGATTCGCA 1141
Db 1082 TGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTACGCTATCGCGCTCCGATTCGCA 1141
QY 1142 GGCATGCGCTTCTATCGCTTCTTGAACGAGTTCTTCTGAGTT-----TAAC 1189
Db 1142 GGCATGCGCTTCTATCGCTTCTTGAACGAGTTCTTCTGAGTT-----TAAC 1189
QY 1190 AGACCAACAGGTTTCCCTTAGGGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCTA 1249
Db 1202 AGACCAACAGGTTTCCCTTAGGGGATCAATTCG-----CCCGCCCGCTA 1250
QY 1250 ACCTTACTGCGGAGCGCTTGGATAGGCGGCTGTGCTTATATGTTATTTT 1309
Db 1251 ACCTTACTGCGGAGCGCTTGGATAGGCGGCTGTGCTTATATGTTATTTT 1310
QY 1310 CCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACTGCGCTTCTTTGA 1369
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Db 1311 CCACCATATTGCGCTTTTGGCAATGTGAGGGGCCCGAAACCTTGGCCCTGTCTTCTTGA 1370
QY 1370 CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTCG 1429
Db 1371 CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTCG 1430
QY 1430 TGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAACAAACGCTCTGTAGCAGCCCTTT 1489
Db 1431 TGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAACAAACGCTCTGTAGCAGCCCTTT 1490
QY 1490 GCAGGAGGGAACCCCGCCACCTGGCGACAGGTGCTCTCGGCGCAAAAGCCAGCTGTAT 1549
Db 1491 GCAGGAGGGAACCCCGCCACCTGGCGACAGGTGCTCTCGGCGCAAAAGCCAGCTGTAT 1550
QY 1550 AAGATACACTGTCAAAGGGCGCAACCCCGCTTCAAGCGTATTCAAGGGGCTGAAGGATGCCAAGG 1609
Db 1551 AAGATACACTGTCAAAGGGCGCAACCCCGCTTCAAGCGTATTCAAGGGGCTGAAGGATGCCAAGG 1610
QY 1610 AAGAGTCAAAATGGCTCTCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAAGG 1669
Db 1611 AAGAGTCAAAATGGCTCTCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAAGG 1670
QY 1670 TACCCATTTGATGGGATCTGATCTGGGCGCTCGGTCACATGCTTTTACATGTTTGTAGT 1729
Db 1671 TACCCATTTGATGGGATCTGATCTGGGCGCTCGGTCACATGCTTTTACATGTTTGTAGT 1730
QY 1730 CGAGTTTAAAAACGCTTAGGCCCCCGAAACCGGAGACGTGTTTCTTTTGAAGAAC 1789
Db 1731 CGAGTTTAAAAACGCTTAGGCCCCCGAAACCGGAGACGTGTTTCTTTTGAAGAAC 1790
QY 1790 ACGATAATACCATG----- 1803
Db 1791 ACGATAATACCATGGAACGGGAGATGCGGAGGCGCGTCTTTCGTAGTTC 1850
QY 1804 ----- 1803
Db 1851 TGATACCTTGTACCTTGTACCGCACTATAAGCTGTTCTCGCTAGGCTCATATGTTGTT 1910
QY 1804 ----- 1803
Db 1911 TACAATATTTTATCACAGGCGCGAGGACACACTTGCAGTGTGGATCCCCCCTCAAG 1970
QY 1804 ----- 1803
Db 1971 TTGGGGGGCGCGATGCGGTCTATCTCTCACTGCGGATCCACCGAGCTAATCT 2030
QY 1804 ----- 1803
Db 2031 TTACCATCACAAAATCTTGTCTGCGCATATCGGTCCACTCATGTTGCTCCAGGCTGATA 2090
QY 1804 ----- 1803
Db 2091 TAAACAAAGTGCCTACTTCTGCGGCGACACGGGCTCATTCGTGATGATGCTGTGTCG 2150
QY 1804 ----- 1803
Db 2151 GGAAGTTGCTGGGGTCAATTATGTCAAAATGCTCTCATGAAGTTGGCGGCACTGACAG 2210
QY 1804 ----- 1803
Db 2211 GTACGTACGTTTATGACCACTCACCCACTGCGGAGCTGGGCGCACGGGGCTACGAG 2270
QY 1804 ----- 1803
Db 2271 ACCTTGGGTGGCAGTTGAGCCGCTGCTTCTCTGATATGAGACCAAGGTTTATCACCT 2330
QY 1804 ----- 1803
Db 2331 GGGGGGAGACACCGCGGCTGTGGGAGCATCATCTTGGGCTGCGCGCTCCGCCGCA 2390
QY 1804 ----- 1803
Db 2391 GGGGAGGAGATACATCTGGGACCGGAGACAGCCTTTGAAGGGGAGGGGTGGCGACTCC 2450

Db	4611	CTGCTCCCGTGTGGAATCCAAGTGGCGGACCTCTGAAGCCTTCTGGCGAAGCATATGT	4670
QY	4022	GGAAATTTCAATCAGCGGGATACAAATATTTAGCAGGCTTTGTCACATCTGCTCTGGCAACCCCG	4081
Db	4671	GGAAATTTCAATCAGCGGGATACAAATATTTAGCAGGCTTTGTCACATCTGCTCTGGCAACCCCG	4730
QY	4082	CGATAGCATCACTGATGGCAATTCACAGCCTCTATCACAGCCGCGCTCACACCCACATATA	4141
Db	4731	CGATAGCATCACTGATGGCAATTCACAGCCTCTATCACAGCCGCGCTCACACCCACATATA	4790
QY	4142	CCCTCTCTTTAAACATCTCTGGGGGATGGGTGGCCGCCAACTTGCTCTCTCCAGCGCTG	4201
Db	4791	CCCTCTCTTTAAACATCTCTGGGGGATGGGTGGCCGCCAACTTGCTCTCTCCAGCGCTG	4850
QY	4202	CTTCTGCTTTTCGTAGGCGCCGCGCATCGCTGGAGCGGCTTTGGCAGCATAGGCTTTGGGA	4261
Db	4851	CTTCTGCTTTTCGTAGGCGCCGCGCATCGCTGGAGCGGCTTTGGCAGCATAGGCTTTGGGA	4910
QY	4262	AGGTGCTTTGTGGATATTTTGGCAGGTATGGAGCAGGGGTGGCAGCGGCTCTGCGGCT	4321
Db	4911	AGGTGCTTTGTGGATATTTTGGCAGGTATGGAGCAGGGGTGGCAGCGGCTCTGCGGCT	4970
QY	4322	TTAAGGTCATGAGCGGCGAGATGGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTTA	4381
Db	4971	TTAAGGTCATGAGCGGCGAGATGGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTTA	5030
QY	4382	TCCCTCTCCCTGGCGCCCTAGCTCGCGGGTCTGTGGCGACGATATCTGCTCGGCACG	4441
Db	5031	TCCCTCTCCCTGGCGCCCTAGCTCGCGGGTCTGTGGCGACGATATCTGCTCGGCACG	5090
QY	4442	TGGGCCACAGGGAGGGGGCTGTGCAGTGGATGAACCGGCTCATAGCGTTCGCTTCGCGGG	4501
Db	5091	TGGGCCACAGGGAGGGGGCTGTGCAGTGGATGAACCGGCTCATAGCGTTCGCTTCGCGGG	5150
QY	4502	GTAACCAACGCTCTCCCCACGCACTATGTGCTGAGAGCGACGCTGCAGCAGTGTCACTC	4561
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Db	5211	AGATCCTCTCTAGTCTTACCATCATCTCAGCTGTGGAAGAGCTTTCACAGTGGATCAACG	5270
QY	4622	AGGACTGTCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGGATATGCA	4681
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QY	4742	TCCCTCTCTCTCATGTCAACGTGGGTAACAAGGAGTCTCGCGGGCGACGGCATCATGC	4801
Db	5391	TCCCTCTCTCTCATGTCAACGTGGGTAACAAGGAGTCTCGCGGGCGACGGCATCATGC	5450
QY	4802	AAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCCATGAGGA	4861
Db	5451	AAACCACTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCCATGAGGA	5510
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QY	4922	CCACGGGCGCTTGACGCCCTCTCCCGGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGTGG	4981
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QY	4982	CTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTTCCACTACGTGAACGGGCATGA	5041
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QY	7322	TCTACGGGGCGCTGTCTACCTTCCATTTGAGCCACTTTGACCTACCTCAGATCAATTCAACGACTCC	7381
Db	7971	TCTACGGGGCGCTGTCTACCTTCCATTTGAGCCACTTTGACCTACCTCAGATCAATTCAACGACTCC	8030
QY	7382	ATGGCTTTAGGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTT	7441
Db	8031	ACGGCTTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTT	8090
QY	7442	CATGCTCAGGAAACTTGGGGTACCGCTTCCAGGTCTGGAGACATCGGGCCAGAAAGTG	7501
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QY	7802	TTCCCTTT	7861
Db	8451	TTCCCTTT	8510
QY	7862	TTTTCTCTTT	7921
Db	8511	TTTTCTCTTT	8570
QY	7922	AGCTGTGAAAGGTCCGTGAGCGCTTCACTGAGAGAGTCTGATCTAGCGCTCTCTGCA	7981
Db	8571	AGCTGTGAAAGGTCCGTGAGCGCTTCACTGAGAGAGTCTGATCTAGCGCTCTCTGCA	8630
QY	7982	GATCAAGT 7989	
Db	8631	GATCAAGT 8638	
RESULT 10			
US-10-029-907-7			
Sequence 7, Application US/10029907			
Patent No. 6706874			
GENERAL INFORMATION:			
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.			
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM			
TITLE OF INVENTION: HEPATITIS C VIRUS			
FILE REFERENCE: 13/083			
CURRENT APPLICATION NUMBER: US/10/029,907			
CURRENT FILING DATE: 2001-12-21			
PRIOR APPLICATION NUMBER: 60/257,857			
PRIOR FILING DATE: 2000-12-22			
NUMBER OF SEQ ID NOS: 25			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 7			
LENGTH: 8638			
TYPE: DNA			
ORGANISM: HCV			
FEATURE:			

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? NAME/KEY: CDS
? LOCATION: (1802)....(8407)
us-10-029-907-7

Query Match      90.7%; Score 7249.8; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7961; Conservative 0; Mismatches 17; Indels 671; Gaps 3;

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Tue Nov 2 14:02:16 2004

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QY	1804	-----	1803	Db	3170	GGTATATGTCTAAGGCACTGGTATCGACCTAACATCAGAACCGGCTAAGGACCATC	3229
Db	2090	ATAACAAAGTCCGCTACTTCTGTCGCGACACGCGCTCATCTGTCATGCTGTG	2149	QY	2581	ACCAAGGTCGCGCTACCTACCTATGCAAGTCTTCTGCGACCGGCTGTG	2640
QY	1804	-----	1803	Db	3230	ACCAAGGTCGCGCTACCTACCTATGCAAGTCTTCTGCGACCGGCTGTG	3289
Db	2150	CGAAGGTTGCTGGGGCTCATTTATGTCCTCAATGCTCTCATGAAAGTTGGCGCATGACA	2209	QY	2641	TCCTGGGGCGCTATGACATCATATATGTAAGTGCCTCACTCACTGACCTGACCACT	2700
QY	1804	-----	1803	Db	3290	TCCTGGGGCGCTATGACATCATATATGTAAGTGCCTCACTCACTGACCTGACCACT	3349
Db	2210	GGTACGTACGTTTATGACCATCTCACCCACTGCGGACCTGGGCCACCGGGCTTACGA	2269	QY	2701	ATCTGGGGCATCGGCACTCTTGACCTCAAGCGGACGCTGGAGCGGACCTGCTGCTG	2760
QY	1804	-----	1803	Db	3350	ATCTGGGGCATCGGCACTCTTGACCTCAAGCGGACGCTGGAGCGGACCTGCTGCTG	3409
Db	2270	GACCTTGGCGTGCAGTTGAGCCCGTCTCTCTCTGATATGAGACCAAGGTTATCACC	2329	QY	2761	CTCGCCACCGCTACCGCTCCGGATCGGTCACTCGTCCCATCATCAAACTCGAGGAGGTG	2820
QY	1804	-----	1803	Db	3410	CTCGCCACCGCTACCGCTCCGGATCGGTCACTCGTCCCATCATCAAACTCGAGGAGGTG	3469
Db	2330	TGGGGGCGACACACCGCGCGTGTGGGACATCATCTTGGGCGTCCCGCTCTCGGCCGC	2389	QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCATCGAGCCATC	2880
QY	1804	-----	1803	Db	3470	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCATCGAGCCATC	3529
Db	2390	AGGGGAGGAGAGATACATCTGGGACCGGACAGACAGCCCTTGAGGCGAGGGTGGGACTC	2449	QY	2881	AAGGGGGAGGAGCACTCATTTTCTGCCATTCGCAAGCAAGCAATCCCATCGAGCCATC	2940
QY	1804	-----	1803	Db	3530	AAGGGGGAGGAGCACTCATTTTCTGCCATTCGCAAGCAAGCAATCCCATCGAGCCATC	3589
Db	2450	CTCGGCTATTAGGCTACTTCCCAACAGACGCGAGGCTTACTTGGCTGCATCATCACC	2509	QY	2941	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTTACCGGGCTTGTATTCGCTC	3000
QY	1861	AGCTCTACGCGCGGACAGGAACAGGTCAGGGGAGGTCGAAGTGTCTCCACCGCA	1920	Db	3590	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTTACCGGGCTTGTATTCGCTC	3649
Db	2510	AGCTCTACGCGCGGACAGGAACAGGTCAGGGGAGGTCGAAGTGTCTCCACCGCA	2569	QY	3001	ATACCAACTAGCGGAGACGTCATTTCTGTAGCAAGCAAGCAATTCGAGCGGCTTTTACC	3060
QY	1921	ACCAATCTTCTCGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCGTGTCC	1980	Db	3650	ATACCAACTAGCGGAGACGTCATTTCTGTAGCAAGCAAGCAATTCGAGCGGCTTTACC	3709
Db	2570	ACCAATCTTCTCGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCGTGTCC	2629	QY	3061	GGCGATTTGCACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTGTGACTCAGC	3120
QY	1981	GGCTCAAGAGCCCTTGGCGGCCAAAGGCGCAATCAACCAATGTACCAATGTGGAC	2040	Db	3710	GGCGATTTGCACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTGTGACTCAGC	3769
Db	2630	GGCTCAAGAGCCCTTGGCGGCCAAAGGCGCAATCAACCAATGTACCAATGTGGAC	2689	QY	3121	CTGACCCGACCTTACCATTTGAGACGACCGCTGCCAAGACGCGGTGTACGCTCG	3180
QY	2041	CAGACCTCTGCTGGTGGAGAGCGCCCGCGGCGCTTCTTGCACACCATGCACTGC	2100	Db	3770	CTGACCCGACCTTACCATTTGAGACGACCGCTGCCAAGACGCGGTGTACGCTCG	3829
Db	2690	CAGGACCTCTGCTGGTGGCAAGCGCCCGCGGCGCTTCTTGCACACCATGCACTGC	2749	QY	3181	CAGCGCGGAGGACGACTGTGTAAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
QY	2101	GGCAGCTCGGACCTTTACTTGTGTACGAGGATGCGGATGTCATTTCCGGTGGCGCGGG	2160	Db	3830	CAGCGCGGAGGACGACTGTGTAAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3889
Db	2750	GGCAGCTCGGACCTTTACTTGTGTACGAGGATGCGGATGTCATTTCCGGTGGCGCGGG	2809	QY	3241	GAAAGCGCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT	3300
QY	2161	GGCGACAGCGGGGAGCTACTTCTCCCGACGCGCTCTCTTGAAGGCTTTTCG	2220	Db	3890	GAAAGCGCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT	3949
Db	2810	GGCGACAGCGGGGAGCTACTTCTCCCGCGCGCTCTCTTGAAGGCTTTTCG	2869	QY	3301	GCTTGTGACGACTCAGCGCCCGCGAGACCTCAGTTAGGTTTGGGGCTTAAACACA	3360
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Db	2870	GGCGGTCATGCTGCTCGCCCTCGGGGACGCTGTGGGCTCTTTCGGGCTGCGGTGTC	2929	QY	3361	CCAGGTTTCCCGCTGTGCGAGGACCATCTGGAGTTTCTGGAGAGCGCTTTTACAGGCTC	3420
QY	2281	ACCGAGGCTTTCGGAAGCGGTGGACTTTTGTATCCCGTCTGAGTCTATGGAACCACTATG	2340	Db	4010	CCAGGTTTCCCGCTGTGCGAGGACCATCTGGAGTTTCTGGAGAGCGCTTTTACAGGCTC	4069
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QY	2341	CGGTCCCGGCTTTCAGGCAACTCGTCCCTCGGCGCTTACCGGACATTTCCAGGTG	2400	Db	4070	ACCGACATGACGCGCTTCTTGTCCGAGCTTAAGCAGGACGAGACAACTTCCCTAC	4129
Db	2990	CGGTCCCGGCTTTCAGGCAACTCGTCCCTCGGCGCTTACCGGACATTTCCAGGTG	3049	QY	3481	CTGCTAGCATACGCGCTTCTTGTCCGAGCTTAAGCAGGACGAGACAACTTCCCTAC	3540
QY	2401	GCCCATCTACGCGCTTTCAGGCAACTCGTCCCTCGGCGCTTACCGGACATTTCCAGGTG	2460	Db	4130	CTGCTAGCATACGCGCTTCTTGTCCGAGCTTAAGCAGGACGAGACAACTTCCCTAC	4189
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QY	2461	GCCCAAGGTTAAGGTTCTTCTCTGAAACCGCTCGTGGCGGACCGCTAGGTTTCGG	2520	Db	4190	CNAATGTGGAAGTGTCTCATACGCTTAAAGCTTACGCTGACGCGGCAAGCGGCTGCTG	4249
Db	3110	GCCCAAGGTTAAGGTTCTTCTCTGAAACCGCTCGTGGCGGACCGCTAGGTTTCGG	3169				

QY	3601	TATAGGCTGGGAGCGGTTTCAAAACGAGGTTACTACCAACACACCCCAATAACCAATACATC	3660	Db	5330	ACGGTGTGACTGATTTTCAAGGCTGGCTCCAGTCCAAGCTCTCTGCGCGGATTCGCGGA	5389
Db	4250	TATAGGCTGGGAGCGGTTTCAAAACGAGGTTACTACCAACACACCCCAATAACCAATACATC	4309	QY	4741	GTCCCTCTTCTCATCTCAACGTTGGGTACAGGAGTCTGGCGGGGCGAGCGGATCATG	4800
QY	3661	ATGGCATGCAATGTGGCTGACCTGGAGTCTGACAGGACCTGGGTCTGGTGGAGGGA	3720	Db	5390	GTCCCTCTTCTCATCTCAACGTTGGGTACAGGAGTCTGGCGGGGCGAGCGGATCATG	5449
Db	4310	ATGGCATGCAATGTGGCTGACCTGGAGTCTGACAGGACCTGGGTCTGGTGGAGGGA	4369	QY	4801	CAAAACACCTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGTTCCATCAGG	4860
QY	3721	GTCTAGCAGCTCTGGCGCGGTATGCTGACAAACAGGACGCTGCTCATTTGGGCGAGG	3780	Db	5450	CAAAACACCTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGTTCCATCAGG	5509
Db	4370	GTCTAGCAGCTCTGGCGCGGTATGCTGACAAACAGGACGCTGCTCATTTGGGCGAGG	4429	QY	4861	ATCGTGGGGCTTAGGACCTCTAGTAACACGTGGCATGGAACATTTCCCAATTAACGCGTAC	4920
QY	3781	ATCATCTTGTCCGGAAGCCCGCATCATTTCCCGACAGGAAAGTCCCTTTACCGGAGTTTC	3840	Db	5510	ATCGTGGGGCTTAGGACCTCTAGTAACACGTGGCATGGAACATTTCCCAATTAACGCGTAC	5569
Db	4430	ATCATCTTGTCCGGAAGCCCGCATCATTTCCCGACAGGAAAGTCCCTTTACCGGAGTTTC	4489	QY	4921	ACCACGGGGCTTGCACGCGCTCCCGGGGCCAAATTTCTAGGGGCTGTGGCGGCTG	4980
QY	3841	GATGATGGAAGAGTGCCTCACACCTCCCTTACATCGAACAGGGAATGACAGCTCGCC	3900	Db	5570	ACCACGGGGCTTGCACGCGCTCCCGGGGCCAAATTTCTAGGGGCTGTGGCGGCTG	5629
Db	4490	GATGATGGAAGAGTGCCTCACACCTCCCTTACATCGAACAGGGAATGACAGCTCGCC	4549	QY	4981	GCTGCTGAGAGTACGTGAGGTTACGCGGTGGGGGATTTCCACTACGTGACGGGCATG	5040
QY	3901	GAACAATTCAAACAGAGGCAATCGGGTTGCTGCAACAGCCCAAGCAAGCGGAGGCT	3960	Db	5630	GCTGCTGAGAGTACGTGAGGTTACGCGGTGGGGGATTTCCACTACGTGACGGGCATG	5689
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QY	3961	GCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTCTGGGCGAAGCATATG	4020	Db	5690	ACCACCTGACAAAGTAAAGTGCCTGTGAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG	5749
Db	4610	GCTGCTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTCTGGGCGAAGCATATG	4669	QY	5101	GATGGGTGGGTTGACACAGGTACGCTCCAGGTGCAACCCCTCTTACGGGAGGAGTTC	5160
QY	4021	TGGAAATTTATCAGCGGGATACAATATTTAGCAGGCTTGTCACTCTGCTGCGCAACCC	4080	Db	5750	GATGGGTGGGTTGACACAGGTACGCTCCAGGTGCAACCCCTCTTACGGGAGGAGTTC	5809
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QY	4081	CGATAGCATCACTGATGGCATTCACAGCTCTATCAACAGCCCGCTCAACACCCCAACAT	4140	Db	5810	ACATTTCTGGTGGGCTCAATCAATPACCTGTGGGTCAACGCTCCCATGCCAGCCGAA	5869
Db	4730	CGATAGCATCACTGATGGCATTCACAGCTCTATCAACAGCCCGCTCAACACCCCAACAT	4789	QY	5221	CGGACGTAGCAGTCTCACTTCCATGTCTACCGACCCCTCCCACTTACGGCGGAGACG	5280
QY	4141	ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGCCGCAACTTGTCTTCCACAGCCT	4200	Db	5870	CTGGACGTAGCAGTCTCACTTCCATGTCTACCGACCCCTCCCACTTACGGCGGAGACG	5929
Db	4790	ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGCCGCAACTTGTCTTCCACAGCCT	4849	QY	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCGAGTCACTAGCTAGCCAG	5340
QY	4201	GCTTCTGCTTTCGAGGCGCGCATCGCTCGAGCGGCTGTGGCAGGAGGCTTGGG	4260	Db	5930	GCTAAGCTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCGAGTCACTAGCTAGCCAG	5989
Db	4850	GCTTCTGCTTTCGAGGCGCGCATCGCTCGAGCGGCTGTGGCAGGAGGCTTGGG	4909	QY	5341	CTGTCTGGCTTCTTGAAGGCAACATGCACTACCGTCTATGACTCCCGGAGCGTAC	5400
QY	4261	AAGTGTCTTGGATATTTGGCAGGTTATGGAGAGGGGTGGCAGGCGCTCGTGCC	4320	Db	5990	CTGTCTGGCTTCTTGAAGGCAACATGCACTACCGTCTATGACTCCCGGAGCGTAC	6049
Db	4910	AAGTGTCTTGGATATTTGGCAGGTTATGGAGAGGGGTGGCAGGCGCTCGTGCC	4969	QY	5401	CTCATCAGGCGCAACCTCTCTGGCGCAGAGATGGCGGGGAAATCATCCCGCTGGAG	5460
QY	4321	TTTAAAGTTCATGAGCGCGGAGATGCCCTCCACGAGGACCTGTTAACCCTACTCCCTGCT	4380	Db	6050	CTCATCAGGCGCAACCTCTCTGGCGCAGAGATGGCGGGGAAATCATCCCGCTGGAG	6109
Db	4970	TTTAAAGTTCATGAGCGCGGAGATGCCCTCCACGAGGACCTGTTAACCCTACTCCCTGCT	5029	QY	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTCAGCGCGCTCCAGGAAATTCCTCGAGCGATG	5520
QY	4381	ATCCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGCGCAGGATGAAACCGGCTGATGCGG	4440	Db	6110	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTCAGCGCGCTCCAGGAAATTCCTCGAGCGATG	6169
Db	5030	ATCCTCTCCCTGGCGCCCTAGTCTGCTGGGCTGCTGCGGCTGCTGCGCAGGATGAAACCGGCTGATGCGG	5089	QY	5521	AGGAAAGTATCCGTTCCCGCGGAGATCTTGGACTCTTTCAGCGCGCTCCAGGAAATTCCTCGAGCGATG	5580
QY	4441	GTGGGCCACAGGGAGGGGCTGTGCAATGATGAAACCGGCTGATGCGGTTCCGCTTCCGCG	4500	Db	6170	AGGAAAGTATCCGTTCCCGCGGAGATCTTGGACTCTTTCAGCGCGCTCCAGGAAATTCCTCGAGCGATG	6229
Db	5090	GTGGGCCACAGGGAGGGGCTGTGCAATGATGAAACCGGCTGATGCGGTTCCGCTTCCGCG	5149	QY	5581	CCCATATGGCAGCCCGGATTAACACCTCCACTGTTAGAGTCTTGGAGGACCCCGGAC	5640
QY	4501	GGTAAACACGCTCTCCCGCACGCACTATGCTGAGAGGCTTCCACAGTGGATCAAC	4560	Db	6230	CCCATATGGCAGCCCGGATTAACACCTCCACTGTTAGAGTCTTGGAGGACCCCGGAC	6289
Db	5150	GGTAAACACGCTCTCCCGCACGCACTATGCTGAGAGGCTTCCACAGTGGATCAAC	5209	QY	5641	TACGTCCTTCCAGTGTACACCGGTGCTCATTTGCCCTGCCAGCCCTCGGATCAAC	5700
QY	4561	CAGATCTCTAGTCTTACCACTACTGCTGAGAGGCTTCCACAGTGGATCAAC	4620	Db	6290	TACGTCCTTCCAGTGTACACCGGTGCTCATTTGCCCTGCCAGCCCTCGGATCAAC	6349
Db	5210	CAGATCTCTAGTCTTACCACTACTGCTGAGAGGCTTCCACAGTGGATCAAC	5269	QY	5701	CTTCCACGGAAGAGGACGCTTGTCTGTGAGAAATCTTACCGTGTCTTCTCCCTTGGCG	5760
QY	4621	GAGGACTGCTCCACGCACTGCTCCGCTCGTGGCTAAGAGATGTTGGGATTTGGATGTC	4680	Db	6350	CTTCCACGGAAGAGGACGCTTGTCTGTGAGAAATCTTACCGTGTCTTCTCCCTTGGCG	6409
Db	5270	GAGGACTGCTCCACGCACTGCTCCGCTCGTGGCTAAGAGATGTTGGGATTTGGATGTC	5329	QY	5761	GAGCTCGCCCAACAGACCTTCGGCAGCTTCGAAATCGTTCGGCGCTCCAGCGGACGCGCA	5820
QY	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAGCTCTCGCGCGATTTGCCGGA	4740				


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QY 7981 AGATCAAGT 7989
Db 8630 AGATCAAGT 8638

RESULT 11
US-10-029-907-25
; Sequence 25, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PENDING FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)....(8407)
US-10-029-907-25

Query Match 90.7%; Score 7248.8; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7960; Conservative 0; Mismatches 17; Indels 671; Gaps 3;

QY 2 CCAGCCCCGAGTGGGGCGACATCCACAPAGATCACTCCCTGTGAGGAACACTACTGT 61
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QY 62 CTTACGCGAGAAAGCTCTAGCCATGGCGTTAGTATGATGTGTCGACGCTCCAGGACC 121
Db 62 CTTACGCGAGAAAGCTCTAGCCATGGCGTTAGTATGATGTGTCGACGCTCCAGGACC 121

QY 122 CCCCCTCCCGGAGAGCAATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCHAG 181
Db 122 CCCCCTCCCGGAGAGCAATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCHAG 181

QY 182 ACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCGCTGAGATTTGGGCGTCCCGCG 241
Db 182 ACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCGCTGAGATTTGGGCGTCCCGCG 241

QY 242 CGAGACTGTAGCGAGTGTGGTTCGGGAAGGCTTGTGTTACTGCTGATAGGG 301
Db 242 CGAGACTGTAGCGAGTGTGGTTCGGGAAGGCTTGTGTTACTGCTGATAGGG 301

QY 302 TGTCTGAGTGTCCCGGAGGCTCTGTAGACGCTGACCATGAGCAAGTCTTAACC 361
Db 302 TGTCTGAGTGTCCCGGAGGCTCTGTAGACGCTGACCATGAGCAAGTCTTAACC 361

QY 362 TCAAGAAACCAAGAGGCGCGCATGTATGAAACAAAGTGTGACGCGAGTCTCC 421
Db 362 TCAAGAAACCAAGAGGCGCGCATGTATGAAACAAAGTGTGACGCGAGTCTCC 421

QY 422 GCGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGACACAGCAATCGGCTC 481
Db 422 GCGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGACACAGCAATCGGCTC 481

QY 482 TGATCGCGCGTGTTCGGGTGTGAGGAGGCGCGCGTCTTTTGTGTCAGACCGA 541
Db 482 TGATCGCGCGTGTTCGGGTGTGAGGAGGCGCGCGTCTTTTGTGTCAGACCGA 541

QY 542 CTTGTCGGTGCCTGAATGAACCTGACGAGGCGCGCGTCTTTTGTGTCAGACCGA 601
Db 542 CTTGTCGGTGCCTGAATGAACCTGACGAGGCGCGCGTCTTTTGTGTCAGACCGA 601

QY 602 GACGGCGTTCCTTGGCGAGCTGTCTGACGCTTGTCTCACTGAAGCGGAAAGGACTGCT 661
Db 602 GACGGCGTTCCTTGGCGAGCTGTCTGACGCTTGTCTCACTGAAGCGGAAAGGACTGCT 661

QY 662 GCTATTGGGCGAAGTGCAGGAGGATCTCTGTCATCTCACTTGTCTCTGCGGAGAA 721
Db 662 GCTATTGGGCGAAGTGCAGGAGGATCTCTGTCATCTCACTTGTCTCTGCGGAGAA 721

QY 722 AGTATCCATCATGGCTGATGCAATGCGGGCTGCAATGCTTGTGATCCGCTACCTGCC 781
Db 722 AGTATCCATCATGGCTGATGCAATGCGGGCTGCAATGCTTGTGATCCGCTACCTGCC 781

QY 782 ATTGACACCAAGCGAATCATGCAATGCGAGGACGCTACTCGATGGAAGCGGCTCT 841
Db 782 ATTGACACCAAGCGAATCATGCAATGCGAGGACGCTACTCGATGGAAGCGGCTCT 841

QY 842 TGTGATCAGGATGATCTGCAAGAGCATCAGGGGCTCGGCGCAGCGGCTGTCG 901
Db 842 TGTGATCAGGATGATCTGCAAGAGCATCAGGGGCTCGGCGCAGCGGCTGTCG 901

QY 902 CAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCGTCTGACCCATGGCGATGCCCTG 961
Db 902 CAGGCTCAAGCGCGCATGCCGAGCGGAGGATCTCGTCTGACCCATGGCGATGCCCTG 961

QY 962 CTTGCGGAATATCATGGTGGAAATGGCGGCTTTCTGGAATTCATCGACTGTGGCGGCT 1021
Db 962 CTTGCGGAATATCATGGTGGAAATGGCGGCTTTCTGGAATTCATCGACTGTGGCGGCT 1021

QY 1022 GGGTGTGGCGACCGCTATCAGGACATAGCGTGTGGCTACCGTGTGATATGCTGAAGCT 1081
Db 1022 GGGTGTGGCGACCGCTATCAGGACATAGCGTGTGGCTACCGTGTGATATGCTGAAGCT 1081

QY 1082 TGGCGCGAATGGGCTGACCGCTTCTGTCGTTTACGCTATGCGCGCTCCGATTCGCA 1141
Db 1082 TGGCGCGAATGGGCTGACCGCTTCTGTCGTTTACGCTATGCGCGCTCCGATTCGCA 1141

QY 1142 GCGCATCGCTTCTATCGCTTCTGACGAGTCTTCTGAGTT-----TAAAC 1189
Db 1142 GCGCATCGCTTCTATCGCTTCTGACGAGTCTTCTGAGTT-----TAAAC 1189

QY 1190 AGACCAACAAAGTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCGCTA 1249
Db 1202 AGACCAACAAAGTTCCTCTAGCGGATCAATTCGCG-----CCCGCCCGCTA 1250

QY 1250 ACCTTACTGCGCGAAGCGCTTGGAAATAGCGCGTGTGGCTTGTCTATATGTTATTT 1309
Db 1251 ACCTTACTGCGCGAAGCGCTTGGAAATAGCGCGTGTGGCTTGTCTATATGTTATTT 1310

QY 1310 CCACCATATTCGCTTCTTGGCAATGAGGCGCGGAAACCTGCGCCCTGTCTTCTGA 1369
Db 1311 CCACCATATTCGCTTCTTGGCAATGAGGCGCGGAAACCTGCGCCCTGTCTTCTGA 1370

QY 1370 CGAGCATTCCTAGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGCTCTGTAATGTCG 1429
Db 1371 CGAGCATTCCTAGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGCTCTGTAATGTCG 1430

QY 1430 TGAAGGAAGGCTTCTCTGGAAGTCTTGAAGCAACAACTGTGACGACCGCTTT 1489
Db 1431 TGAAGGAAGGCTTCTCTGGAAGTCTTGAAGCAACAACTGTGACGACCGCTTT 1490

QY 1490 GCAGGCGAGCGGACCGCCCGCTGCGAGAGGCTCTGCGCCCAAGCGCTAT 1549
Db 1491 GCAGGCGAGCGGACCGCCCGCTGCGAGAGGCTCTGCGCCCAAGCGCTAT 1550

QY 1550 AAGATACACTGCAAGGCGGACCAACCGCTGCGAGAGGCTCTGCGCCCAAGCGCTAT 1609
Db 1551 AAGATACACTGCAAGGCGGACCAACCGCTGCGAGAGGCTCTGCGCCCAAGCGCTAT 1610

QY 1610 AAGAGTCAATGGCTCTCTCAAGGCTATTCAAGAGGCTTGAAGGATGCCCAAGG 1669
Db 1611 AAGAGTCAATGGCTCTCTCAAGGCTATTCAAGAGGCTTGAAGGATGCCCAAGG 1670

QY 1670 TACCCCAATGATGGATCTGATCTGGGCGCTCGGTCATGCTTTTACATGTTTACT 1729
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Db	1671	TACCCCAATGATGGATCTGATCTGGGGCTCGGTGCACATGCTTACATGCTTTAGT	1730	2751	GGAGTCGGACCTTTACTTGTGTGTCAGAACATGCCGATGTCATTCCTCGGTGCGCGCGGG	2810
Qy	1730	CGAGGTTAAAAACGCTAGGCCCCCGAACACACGGGGACGTGTTTCTTTGAAAAAC	1789	2162	CGCAGCAGGGGAGCCCTACTCTCCCAAGCCCGTCTCTACTTTGAAGGCTCTTCGG	2221
Db	1731	CGAGGTTAAAAACGCTAGGCCCCCGAACACACGGGGACGTGTTTCTTTGAAAAAC	1790	2811	GGCAGCAGGGGAGCCCTACTCTCCCGCGCCGCTCTCTACTTTGAAGGCTCTTCGG	2870
Qy	1790	ACGATAATACCATG-----	1803	2222	GGGTCCTCTGCTCTGCGGCTCGGGGACGCTGTGGGCACTTTTGGGGCTGCGGTGTGCA	2281
Db	1791	ACGATAATACCATGACCGGGAGATGGCAGCATCGTGGGAGCGCGGTTTTCGTAGGTC	1850	2871	GGGTCCTCTGCTCTGCGGCTCGGGGACGCTGTGGGCACTTTTGGGGCTGCGGTGTGCA	2930
Qy	1804	-----	1803	2282	CCGAGGGGTTCCGAAGCGGTGGACTTTGTATACCGTTCGAGTCTATGGAACCACTATGC	2341
Db	1851	TGATACTCTTGACTTGTCAACGCACTATAAGCTGTTCTCTCGTAGGCTCATATGCTGT	1910	2931	CCGAGGGGTTCCGAAGCGGTGGACTTTGTATACCGTTCGAGTCTATGGAACCACTATGC	2990
Qy	1804	-----	1803	2342	GGTCCCGGCTTTTCACGCAAACTCGTCCCTTCGCGCCGTAACGAGACATTCACAGTGG	2401
Db	1911	TACATAATTTATCACAGGGCGGAGGACACTTGCAGTGTGGATCCCGCCCTCAACG	1970	2991	GGTCCCGGCTTTTCACGCAAACTCGTCCCTTCGCGCCGTAACGAGACATTCACAGTGG	3050
Qy	1804	-----	1803	2402	CCCATCTACAGCCCTACTCTGGTAGCGCAAGAGCACTAAGGTGCGCGCTGCGTATGCAG	2461
Db	1971	TTCCGGGGGCGCGATCGCGTCATCTCTCACTCGTGGCGATCCACCGAGCTAATCT	2030	3051	CCCATCTACAGCCCTACTCTGGTAGCGCAAGAGCACTAAGGTGCGCGCTGCGTATGCAG	3110
Qy	1804	-----	1803	2462	CCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGGTGCGCGCAACCTAGGTTTCGGG	2521
Db	2031	TTACCATCACCAAAUCTTGCTGCGCATACTCGGTCCACTCATGCTGCTCCAGGCTGTA	2090	3111	CCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGGTGCGCGCAACCTAGGTTTCGGG	3170
Qy	1804	-----	1803	2522	CGTATATGCTTAAGGACACATGCTATCGACCCCTAACATCAGAACCGGGGTAAAGACCATCA	2581
Db	2091	TAACCAAGTGCCGTACTCTGTGCGCGCACAGGGCTCAATTGCTGATGATGCTGTGCT	2150	3171	CGTATATGCTTAAGGACACATGCTATCGACCCCTAACATCAGAACCGGGGTAAAGACCATCA	3230
Qy	1804	-----	1803	2582	CCAGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTGCGCAAGGTGCTGCT	2641
Db	2151	GGAGGTTGCTGGGGTCAATTATGTCAAATGGCTCTCATGAAGTTGGCCGCACTGACAG	2210	3231	CCAGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTGCGCAAGGTGCTGCT	3290
Qy	1804	-----	1803	2642	CTGGGGCGCTATGACATCATATATGTGATGAGTGCCTCAACTGACCTGACCCACTA	2701
Db	2211	GTACGTAGTTTATGACCAATCTACCCCACTGCGGGACTGGGCCACGCGGGCTACGAG	2270	3291	CTGGGGCGCTATGACATCATATATGTGATGAGTGCCTCAACTGACCTGACCCACTA	3350
Qy	1804	-----	1803	2702	TCCTGGGCATCGGCACAGTCTCTGCAACAGCGGAGAGCGGTGGAGCGGACTCGCTGTC	2761
Db	2271	ACCTTGGCGGTGGCAGTTGAGCCCGTCTGCTCTCTGATGATGGAGACCAAGTTTACCT	2330	3351	TCCTGGGCATCGGCACAGTCTCTGCAACAGCGGAGAGCGGTGGAGCGGACTCGCTGTC	3410
Qy	1804	-----	1803	2762	TCGCCACCGCTACCGCTCCGGGATCGGTCAACGTGCGCATCCAAACATCGAGAGGTGG	2821
Db	2331	GGGGGCGAGACACCGCGCGTGTGGGACATCATCTTGGGCTGCGCGTCCCGCCGCA	2390	3411	TCGCCACCGCTACCGCTCCGGGATCGGTCAACGTGCGCATCCAAACATCGAGAGGTGG	3470
Qy	1804	-----	1803	2822	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATTCGAGACCATCA	2881
Db	2391	GGGGGAGGAGATACATCTGGGACCGGACAGAGCTTTGAAGGGCAGGGTGGGACTCC	2450	3471	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATTCGAGACCATCA	3530
Qy	1804	--GCGCCTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCTA	1861	2882	AGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAGAAATGTGATGAGCTCGCGCGA	2941
Db	2451	TCGGGCTTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCA	2510	3531	AGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAGAAATGTGATGAGCTCGCGCGA	3590
Qy	1862	GCTTCACAGCGCGGACAGAACAGGTGCGAGGGGAGGTCCAGGTGCTCCACCGCAA	1921	2942	AGCTGTCCGGCTCCGAGCTCAATGCTGTAGCATATTACCGGGCTTGAATGATCCGTCA	3001
Db	2511	GCTTCACAGCGCGGACAGAACAGGTGCGAGGGGAGGTCCAGGTGCTCCACCGCAA	2570	3591	AGCTGTCCGGCTCCGAGCTCAATGCTGTAGCATATTACCGGGCTTGAATGATCCGTCA	3650
Qy	1922	CACATCTTCTGCGGACTGCTGCTCAATGGGCTGTGTTGGACTGTCTATCATGTTGCGG	1981	3002	TACCAACTAGCGGAGACGTCTTGTGCTAGCAACCGAGCGCTCTAATGACGGGCTTTACCG	3061
Db	2571	CACATCTTCTGCGGACTGCTGCTCAATGGGCTGTGTTGGACTGTCTATCATGTTGCGG	2630	3651	TACCAACTAGCGGAGACGTCTTGTGCTAGCAACCGAGCGCTCTAATGACGGGCTTTACCG	3710
Qy	1982	GCTCAAGACCTTTCGCGGCCAAAGGGCCCAATCAACCAATGTACCAATGTGGACC	2041	3062	GGGATTTCCAGTTCAGTGTGATGCTGCAATACATGTGTACCCAGACAGTCTGAGCTCAGCC	3121
Db	2631	GCTCAAGACCTTTCGCGGCCAAAGGGCCCAATCAACCAATGTACCAATGTGGACC	2690	3711	GGGATTTCCAGTTCAGTGTGATGCTGCAATACATGTGTACCCAGACAGTCTGAGCTCAGCC	3770
Qy	2042	AGGACCTGCTGCTGCGAGCGCCCCCGGGCGGCTTCTTTGACACCAATGACCTGCG	2101	3122	TGGACCCGACCTTCAACATTTGAGACCGACCGCTGCGCAACAGACCGGCTGTCACGCTGC	3181
Db	2691	AGGACCTGCTGCTGCGAGCGCCCCCGGGCGGCTTCTTTGACACCAATGACCTGCG	2750	3771	TGGACCCGACCTTCAACATTTGAGACCGACCGCTGCGCAACAGACCGGCTGTCACGCTGC	3830
Qy	2102	GCAGCTCGGACCTTTTACTTGTGTACAGAGGATGCGGATGTCATTCGGTGGCGGGGG	2161	3182	AGCGGCGAGGACGAGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGAG	3241
Qy				3831	AGCGGCGAGGACGAGCTGGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGAG	3890

[illegible]

QY 7622 TATCCAGCTGGTTCGTGCTGTTACAGCGGGGAGACATATATCAAGAGCTGTCTCGTG 7681
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QY 8271 TATCCAGCTGGTTCGTGCTGTTACAGCGGGGAGACATATATCAAGAGCTGTCTCGTG 8330
Db |||||
QY 7682 CCCGACCCCGCTGGTTCATGTGGTGGCTACTCCCTACTTCTGTAGGGTAGGCATCTATC 7741
Db |||||
QY 8331 CCCGACCCCGCTGGTTCATGTGGTGGCTACTCCCTACTTCTGTAGGGTAGGCATCTATC 8390
QY 7742 TACTCCCGCAACCATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTT 7801
Db |||||
QY 8391 TACTCCCGCAACCATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTT 8450
QY 7802 TTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7861
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QY 8451 TTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8510
QY 7862 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7921
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QY 8511 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8570
QY 7922 AGCTGTAAAGTCCGTGAGCGCTTGACTGCAGAGAGTGTCTGATCTGGCCCTCTGCA 7981
Db |||||
QY 8571 AGCTGTAAAGTCCGTGAGCGCTTGACTGCAGAGAGTGTCTGATCTGGCCCTCTGCA 8630
QY 7982 GATCAAGT 7989
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QY 8631 GATCAAGT 8638

RESULT 12

US-10-029-907-2
; Sequence 2, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8642
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
; NAME/KEY: variation
; LOCATION: 6268
; OTHER INFORMATION: r = a or g
; NAME/KEY: variation
; LOCATION: 4446
; OTHER INFORMATION: r = a or g
US-10-029-907-2

Query Match 90.7%; Score 7246.8; DB 4; Length 8642;
Best Local Similarity 92.1%; Pred.No. 0;
Matches 7966; Conservative 2; Mismatches 9; Indels 675; Gaps 4;
QY 2 CCAGCCCCCGATTGGGGGACACTCCACATAGATCACTCCCTCTGTAGGAACTACTGT 61
Db |||||
QY 2 CCAGCCCCCGATTGGGGGACACTCCACATAGATCACTCCCTCTGTAGGAACTACTGT 61
Db |||||
QY 62 CTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAGCCCTCCAGGACC 121
Db |||||
QY 62 CTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAGCCCTCCAGGACC 121
Db |||||
QY 122 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACGGGTGAGTACACCGGAATTGCCAGG 181
Db |||||

Db |||||
QY 122 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG 181
QY 182 ACGACCGGGTCCCTTTCTTGGATCAACCCCGCTCAATGCCTGGAGATTGGGCGTCCCCCG 241
Db |||||
QY 182 ACGACCGGGTCCCTTTCTTGGATCAACCCCGCTCAATGCCTGGAGATTGGGCGTCCCCCG 241
QY 242 CGAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGCCCTTGTGGTACTGCCTGTATAGGG 301
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QY 242 CGAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGCCCTTGTGGTACTGCCTGTATAGGG 301
QY 302 TGTCTGCGAGTCCCGCGGAGGTCTCTAGACGCTGACCATGAGACGAACTCTAAACC 361
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QY 302 TGTCTGCGAGTCCCGCGGAGGTCTCTAGACGCTGACCATGAGACGAACTCTAAACC 361
QY 362 TCAAGAAAAAACAAGGGCGCGCATGATTGAAACAAGATGATTGACGCGAGGTCTCC 421
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QY 362 TCAAGAAAAAACAAGGGCGCGCATGATTGAAACAAGATGATTGACGCGAGGTCTCC 421
QY 422 GSCCGCTTGGGTGAGAGGCTATTCCGGCTATGACTGGGCACAAACAGCAATCGGCTGCTC 481
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QY 422 GSCCGCTTGGGTGAGAGGCTATTCCGGCTATGACTGGGCACAAACAGCAATCGGCTGCTC 481
QY 482 TGATGCCCGCGTGTTCGGCTGTACGCGCAGGGGCGCGGTTCTTTTGTCAAGACCGA 541
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QY 482 TGATGCCCGCGTGTTCGGCTGTACGCGCAGGGGCGCGGTTCTTTTGTCAAGACCGA 541
QY 542 CCTGTCCGGTCCCTGAAATGAATGCACTGACGACGAGCGCGGCTATCGTGGCTGGCCAC 601
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QY 542 CCTGTCCGGTCCCTGAAATGAATGCACTGACGACGAGCGCGGCTATCGTGGCTGGCCAC 601
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QY 602 GACGGGCTTCCCTTGGCGAGCTGTCTCGAGCTGTCTCACTGAAGCGGAAAGGAGCTGGCT 661
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QY 722 AGTATCCATCATGCTGATGCAATGCGGCGGCTCATACGCTTGATCGGCTACTGGCC 781
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QY 782 ATTGCGACCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTCT 841
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QY 782 ATTGCGACCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTCT 841
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Db |||||
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QY 902 CAGGCTCAAGGGCGCATGCCGCGAGGATCTCTGTCGACCCATCGCGAGCTGCTG 961
Db |||||
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QY 962 CTTGCGGAATATCATGCTGGAATAAAGCGCGCTTTCTGGAATTCATCGACTGTGGCGGCT 1021
Db |||||
QY 962 CTTGCGGAATATCATGCTGGAATAAAGCGCGCTTTCTGGAATTCATCGACTGTGGCGGCT 1021
QY 1022 GGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGGTGATTTGCTGGAAGCT 1081
Db |||||
QY 1022 GGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGGTGATTTGCTGGAAGCT 1081
QY 1082 TGGCGCGGAATGGGCTGACCGCTTCTCTGCTTTTACCGTATCGCGCTCCCGATTGCGA 1141
Db |||||
QY 1082 TGGCGCGGAATGGGCTGACCGCTTCTCTGCTTTTACCGTATCGCGCTCCCGATTGCGA 1141
QY 1142 GGGATCGCTTCTATCGCTTCTTACGAGTCTTCTCTGAGTT-----TAAAC 1189
Db |||||
QY 1142 GGGATCGCTTCTATCGCTTCTTACGAGTCTTCTCTGAGTT-----TAAAC 1189
QY 1190 AGACCACACCGGTTTCCCTCTAGCGGAGTCAATTCCGCCCTCTCCCTCCCCCCCCCTA 1249
Db |||||

Db	1202	AGACCAACACGGTTTCCTCTAGCGGATCAATTCG-----CCCCCCCCCTA	1250
Qy	1250	ACGTTACTGGCCGAAGCCGCTTGGAAATAAGCCGGTGTGCGTTGTCTATATGTTATTTT	1309
Db	1251	ACGTTACTGGCCGAAGCCGCTTGGAAATAAGCCGGTGTGCGTTGTCTATATGTTATTTT	1310
Qy	1310	CCACCATATTCGCTTCTTTGGCAATGTAGGCCCCGGAACCTGCTCTCTTTGA	1369
Db	1311	CCACCATATTCGCTTCTTTGGCAATGTAGGCCCCGGAACCTGCTCTCTTTGA	1370
Qy	1370	CGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCG	1429
Db	1371	CGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCG	1430
Qy	1430	TGAAGGAAGCAGTTCCTCTGGAAGTCTTTGAAGACAAACAACGCTGTAGCGACCTTTT	1489
Db	1431	TGAAGGAAGCAGTTCCTCTGGAAGTCTTTGAAGACAAACAACGCTGTAGCGACCTTTT	1490
Qy	1490	GCAGGACGGGAACCCCTCTGCGGACAGGTGCTCTGCGCCAAAGCCACGTTGAT	1549
Db	1491	GCAGGACGGGAACCCCTCTGCGGACAGGTGCTCTGCGCCAAAGCCACGTTGAT	1550
Qy	1550	AGATACACCTGCAAGGGGCAACACCCAGTGCACGTTGTGAGTTGGATGTTGG	1609
Db	1551	AGATACACCTGCAAGGGGCAACACCCAGTGCACGTTGTGAGTTGGATGTTGG	1610
Qy	1610	AAAGAGTCAAAATGGCTCTCTCAAGGGTATTCAAACAAAGGGCTGAAGGATGCCAGAAG	1669
Db	1611	AAAGAGTCAAAATGGCTCTCTCAAGGGTATTCAAACAAAGGGCTGAAGGATGCCAGAAG	1670
Qy	1670	TACCCCATTTGATGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTGTAGT	1729
Db	1671	TACCCCATTTGATGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTGTAGT	1730
Qy	1730	CGAGTTTAAAGAGCTAGCGCCCGGAAACCAAGGGAGTGGTTTCTTTGAAAGAAC	1789
Db	1731	CGAGTTTAAAGAGCTAGCGCCCGGAAACCAAGGGAGTGGTTTCTTTGAAAGAAC	1790
Qy	1790	ACGATAATACCATG-----	1803
Db	1791	ACGATAATACCATGACCGGAGATGGCGATCGTGGAGGCGCGTTTTCGTAGGTC	1850
Qy	1804	-----	1803
Db	1851	TGATACTTTGACCTTTGTACCGCACTATAAGCTGTTCTCGTAGGCTCATATGTTGTT	1910
Qy	1804	-----	1803
Db	1911	TACAATATTTTATCACAGGCGGAGGACACTTGCAGTGTGGATCCCCCTCAACG	1970
Qy	1804	-----	1803
Db	1971	TTGCGGGGGCGGATGCGCTCATCTCTCACGTGGCGGATCCACCCAGAGTAACTCT	2030
Qy	1804	-----	1803
Db	2031	TTACCATCAACCAAAATCTTGTCTGCCATACCTCGGTCCACTCATGTGCTCCAGGCTGTA	2090
Qy	1804	-----	1803
Db	2091	TAACCAAGTGGCTACTTCTGTCGGGACACAGGGCTCATTCGTGATGATGCTGTTGTC	2150
Qy	1804	-----	1803
Db	2151	GGAGGTTGCTGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCGGCTGACAG	2210
Qy	1804	-----	1803
Db	2211	GTACGTACGTTTATGACATCTCACCCACTGCGGACTGGGCGGACGCGGGCTACGAG	2270
Qy	1804	-----	1803
Db	2271	ACCTTGGGTGGAGTTGAGCCCGTCTCTCTGTATGATGAGACCAAGGTTATCATCT	2330
Qy	1804	-----	1803
Db	2331	GGGGGCGAGACACCGCGGCTGTGGGACATCATCTTTGGGCTGCGCGTCTCGCCCGCA	2390
Qy	1804	-----	1803
Db	2391	GGGGGAGGAGATACATCTGGGACCGGACAGCCTTGAAGGGCAGGGTGGGACTCC	2450
Qy	1804	-----	1803
Db	2451	TCGCGCTTATACGGCTTACTCCCAACAGAGCGGAGGCTACTTTGGCTGCACTCATCTA	2510
Qy	1861	TCGCGCTTATACGGCTTACTCCCAACAGAGCGGAGGCTACTTTGGCTGCACTCATCTA	2510
Db	1862	GCCTCACAGCGCGGACAGGAACCAAGGTCTGAGGGGAGGTCCCAAGTGTCTCCACCGCAA	1921
Qy	2511	GCCTCACAGCGCGGACAGGAACCAAGGTCTGAGGGGAGGTCCCAAGTGTCTCCACCGCAA	2570
Db	1922	CACATCTTTCTGCGGACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGG	1981
Qy	2571	CACATCTTTCTGCGGACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGG	2630
Db	1982	GCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGCGAC	2041
Qy	2631	GCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGCGAC	2090
Db	2042	AGGACCTCTGCGCTGGCAAGCGCCCCCGGGCGGTTCTTTGACACCAATGACCTGCG	2101
Qy	2691	AGGACCTCTGCGCTGGCAAGCGCCCCCGGGCGGTTCTTTGACACCAATGACCTGCG	2750
Db	2102	GCAGCTCGGACCTTACTTGTTCAGAGGATCCCGGATGTCTTCGGTGCAGCGCGGG	2161
Qy	2751	GCAGCTCGGACCTTACTTGTTCAGAGGATCCCGGATGTCTTCGGTGCAGCGCGGG	2810
Db	2162	GCAGACAGCGGGGAGCCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGGCTCTTCGG	2221
Qy	2811	GCAGACAGCGGGGAGCCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGGCTCTTCGG	2870
Db	2222	GCAGTCCACTGCTCTGCGGCGGCGCTGTTGGGCACTTTTCGGGCTGCCGTGTGCA	2281
Qy	2871	GCAGTCCACTGCTCTGCGGCGGCGCTGTTGGGCACTTTTCGGGCTGCCGTGTGCA	2930
Db	2282	CCGAGGGGTTCGAAAGCGGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATGC	2341
Qy	2931	CCGAGGGGTTCGAAAGCGGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATGC	2990
Db	2342	GGTCCCGGCTTTCACGGACAACTCTGCCCTCGCGGCTGACCGGATTCAGAGTGG	2401
Qy	2991	GGTCCCGGCTTTCACGGACAACTCTGCCCTCGCGGCTGACCGGATTCAGAGTGG	3050
Db	2402	CCCATCTACAGCGCCCTACTGTTAGCGCAAGAGCACTAAGGTGCCGCTGCGTATGCAG	2461
Qy	3051	CCCATCTACAGCGCCCTACTGTTAGCGCAAGAGCACTAAGGTGCCGCTGCGTATGCAG	3110
Db	2462	CCCAGGGTATAAGGTGCTTCTCTGAAACCGCTCGCTCGCCCACTTCCAGTTCGGGG	2521
Qy	3111	CCCAGGGTATAAGGTGCTTCTCTGAAACCGCTCGCTCGCCCACTTCCAGTTCGGGG	3170
Db	2522	CGTATATGCTTAAGGCAATGATTCGACCTTAACATCAGAACCGGGTGAAGACCATCA	2581
Qy	3171	CGTATATGCTTAAGGCAATGATTCGACCTTAACATCAGAACCGGGTGAAGACCATCA	3230
Db	2582	CCACGGGTGCCCCCATCAGTACTCCACTATGGCAAGTTTCTTCCGACGGTGTGCT	2641
Qy	3231	CCACGGGTGCCCCCATCAGTACTCCACTATGGCAAGTTTCTTCCGACGGTGTGCT	3290
Db	2642	CTGGGGCGCCTTATGACATCAATAATGTAGTGCACCTCACTGATCGACCTA	2701
Qy	3291	CTGGGGCGCCTTATGACATCAATAATGTAGTGCACCTCACTGATCGACCTA	3350
Db	2702	TCCTGGGCAATCGGCAAGTCTTGGACCAAGCGGAGCGGTGGAGCGGACTCGTGTGC	2761
Qy	3351	TCCTGGGCAATCGGCAAGTCTTGGACCAAGCGGAGCGGTGGAGCGGACTCGTGTGC	3410
Db			

Qy	2762	TGCCACCGCTACGCTTCGGGATCGGTCAACGTCACCGTCCACATCCAAACATCGAGAGGTGG	2821
Db	3411	TGCCACCGCTACGCTTCGGGATCGGTCAACGTCACCGTCCACATCCAAACATCGAGAGGTGG	3470
Qy	2822	CNCTGTCAGCACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCA	2881
Db	3471	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCA	3530
Qy	2882	AGGGGGGAGGACCTCATTTTCTGCATTCCAAAGAAATGTGATGAGCTCGCGCGA	2941
Db	3531	AGGGGGGAGGACCTCATTTTCTGCATTCCAAAGAAATGTGATGAGCTCGCGCGA	3590
Qy	2942	AGCTGTCCGGCTCGGATCTCAATGTGTAGCATATTACCGGGCCTTGATGATCCGTCA	3001
Db	3591	AGCTGTCCGGCTCGGATCTCAATGTGTAGCATATTACCGGGCCTTGATGATCCGTCA	3650
Qy	3002	TACCAACTAGCGGAGACGTCATTGTCGTAGCAACGGA	3061
Db	3651	TACCAACTAGCGGAGACGTCATTGTCGTAGCAACGGA	3710
Qy	3062	CGCATTCGACTCAGTGATCGACTGCAATACATGATGTCAACGAGACGTCGACTTCAGGC	3121
Db	3711	CGCATTCGACTCAGTGATCGACTGCAATACATGATGTCAACGAGACGTCGACTTCAGGC	3770
Qy	3122	TGGACCGACCTTACCAATTGAGAGCAACGCTGCCACAAGACGGGTGTCAAGCTCGC	3181
Db	3771	TGGACCGACCTTACCAATTGAGAGCAACGCTGCCACAAGACGGGTGTCAAGCTCGC	3830
Qy	3182	AGCGGGCAGGACGACTCGTATGGGCGAGATGGGCAITTTACAGTTTGTGACTCCAGGAG	3241
Db	3831	AGCGGGCAGGACGACTCGTATGGGCGAGATGGGCAITTTACAGTTTGTGACTCCAGGAG	3890
Qy	3242	AACGGCCCTCGGGCATGTTCAATTCCTCGGTTCTGTGCGAGTGCTATCACGGGGCTGTG	3301
Db	3891	AACGGCCCTCGGGCATGTTCAATTCCTCGGTTCTGTGCGAGTGCTATCACGGGGCTGTG	3950
Qy	3302	CTTGGTACGAGCTACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACAC	3361
Db	3951	CTTGGTACGAGCTACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACAC	4010
Qy	3362	CAGGGTGCCTGTCGACGAGCACTCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTCA	3421
Db	4011	CAGGGTGCCTGTCGACGAGCACTCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTCA	4070
Qy	3422	CCCATATAGACGCCATTTCTTGTCACAGACTAAGCAGGACGAGAGACAATTCCTCCCTACC	3481
Db	4071	CCCATATAGACGCCATTTCTTGTCACAGACTAAGCAGGACGAGAGACAATTCCTCCCTACC	4130
Qy	3482	TGGTAGCATACAGGCTACGGTGTGCGCGAGGCTCAGGCTCCACCTCCATCGTGGACC	3541
Db	4131	TGGTAGCATACAGGCTACGGTGTGCGCGAGGCTCAGGCTCCACCTCCATCGTGGACC	4190
Qy	3542	AAATGTGAAGTGTCTCATACGCTAAAGCTACGCTGACAGGCTCAGGCTCCACCTCCATCGTGGAG	3601
Db	4191	AAATGTGAAGTGTCTCATACGCTAAAGCTACGCTGACAGGCTCAGGCTCCACCTCCATCGTGGAG	4250
Qy	3602	ATAGCTGGAGCGGTTCAAAAACGAGTTTACTACCAACACCCCAATAACCAATATATCA	3661
Db	4251	ATAGCTGGAGCGGTTCAAAAACGAGTTTACTACCAACACCCCAATAACCAATATATCA	4310
Qy	3662	TGGCATGATGTCGGCTGACCTGGAGTGCTCAGAGACCTGGGTGCTGGTAGGCGGAG	3721
Db	4311	TGGCATGATGTCGGCTGACCTGGAGTGCTCAGAGACCTGGGTGCTGGTAGGCGGAG	4370
Qy	3722	TCCTAGCAGCTCTGGCCCGGTAATTCCTTGACAAACAGGACGCTGTCATTGTGGGAGGA	3781
Db	4371	TCCTAGCAGCTCTGGCCCGGTAATTCCTTGACAAACAGGACGCTGTCATTGTGGGAGGA	4430
Qy	3782	TCATCTTGTCCGGAAGCCGCGCATCATTTCCCGACAGGGAAGTCTCTTTACCGGAGTTCC	3841
Db	4431	TCATCTTGTCCGGAAGCCGCGCATCATTTCCCGACAGGGAAGTCTCTTTACCGGAGTTCC	4490
Qy	3842	ATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAAACAGGGAATGCACTCGCGC	3901

Db	4491	ATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAAACAGGGAATGCAGCTCGCGG	4550
QY	3902	AACAATTCAAAACAGAAAGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCTG	3961
Db	4551	AACAATTCAAAACAGAAAGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCTG	4610
QY	3962	CTGCTCCCGTGGTGAATCCAAGTCGCGGACCCCTCGAAGCCTTCTGGGGCAAGCATATGT	4021
Db	4611	CTGCTCCCGTGGTGAATCCAAGTCGCGGACCCCTCGAAGCCTTCTGGGGCAAGCATATGT	4670
QY	4022	GGAATTTCAACAGCGGGGATACAATATTAGCAGGCTTGTCCACTCTGCTGCGACACCCCG	4081
Db	4671	GGAATTTCAACAGCGGGGATACAATATTAGCAGGCTTGTCCACTCTGCTGCGACACCCCG	4730
QY	4082	CGATAGCATCACTGATGCGCATTCACAGCCTCTATCACCAGCCGCTCACCAACCCCAACATA	4141
Db	4731	CGATAGCATCACTGATGCGCATTCACAGCCTCTATCACCAGCCGCTCACCAACCAACATA	4790
QY	4142	CCCTTCCTGTTTAAACATCTCGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCTG	4201
Db	4791	CCCTTCCTGTTTAAACATCTCGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCTG	4850
QY	4202	CTTCTGCTTTCTGTAAGCGCCGGCATCTGTCAGCGGCTGTTGGCAGCATAGGCGCTCGGCA	4261
Db	4851	CTTCTGCTTTCTGTAAGCGCCGGCATCTGTCAGCGGCTGTTGGCAGCATAGGCGCTCGGCA	4910
QY	4262	AGGTGCTGTGGAATATTTTGGCAGGTTATGGAGAGGGTGGCAGGCGCGCTCGTGGCCT	4321
Db	4911	AGGTGCTGTGGAATATTTTGGCAGGTTATGGAGAGGGTGGCAGGCGCGCTCGTGGCCT	4970
QY	4322	TTAAGGTCTAGAGCGCGAGATGCCCTCCACCGAGACCTGGTTAACTACTCCCTGCTA	4381
Db	4971	TTAAGGTCTAGAGCGCGAGATGCCCTCCACCGAGACCTGGTTAACTACTCCCTGCTA	5030
QY	4382	TCCTCTCCCTTGGCGCCCTAGTCTCGGGTCTGTGTCGCGAGGATCTCGTTCGGCAG	4441
Db	5031	TCCTCTCCCTTGGCGCCCTAGTCTCGGGTCTGTGTCGCGAGGATCTCGTTCGGCAG	5090
QY	4442	TGGGCCACAGGGAGGGGGTGTGCACTGGATGAACCGGCTGATAGCGTTTCGGTTTCGGGG	4501
Db	5091	TGGGCCACAGGGAGGGGGTGTGCACTGGATGAACCGGCTGATAGCGTTTCGGTTTCGGGG	5150
QY	4502	GTAACCAAGCTCCCCACGCACTATGTGCTGAGAGCGAGCGCTCGAGCACTGTCACTC	4561
Db	5151	GTAACCAAGCTCCCCACGCACTATGTGCTGAGAGCGAGCGCTCGAGCACTGTCACTC	5210
QY	4562	AGATCCTCTTAGTCTTACCATCACTCACTGCTGAGAGGGCTTCAAGTGGATCAACG	4621
Db	5211	AGATCCTCTTAGTCTTACCATCACTCACTGCTGAGAGGGCTTCAAGTGGATCAACG	5270
QY	4622	AGGACTGTCCAAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTCGATATGCA	4681
Db	5271	AGGACTGTCCAAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTCGATATGCA	5330
QY	4682	CGGTGTTCACTGATTTCAGACCTGGCTCCAGTCCAAGCTCTGCGCGGATTCGCGGAG	4741
Db	5331	CGGTGTTCACTGATTTCAGACCTGGCTCCAGTCCAAGCTCTGCGCGGATTCGCGGAG	5390
QY	4742	TCCCTTCTTCTCATGTCAACGTGGGTACAGGGNGTCTGGCGGGGCGACGCGATCATGC	4801
Db	5391	TCCCTTCTTCTCATGTCAACGTGGGTACAGGGNGTCTGGCGGGGCGACGCGATCATGC	5450
QY	4802	AAACCACTGCCCCATGTGGAGCAGACATCACCGACATGTGAAAAACGGTTTCCATGAGA	4861
Db	5451	AAACCACTGCCCCATGTGGAGCAGACATCACCGACATGTGAAAAACGGTTTCCATGAGA	5510
QY	4862	TCGTGGGGCTAGGACTGTAGTAAACGTGGCATGGAACTTCCCATTAACCGGTACA	4921
Db	5511	TCGTGGGGCTAGGACTGTAGTAAACGTGGCATGGAACTTCCCATTAACCGGTACA	5570
QY	4922	CCAGGSCCCTTCAGCGCCCTCCCGCGCCAAATTAATTCAGGCGCTGTGGCGGTGG	4981

Db	5571	CCACGGGCCCCGTGACAGCCCTCCCGCGGCCCAAAATTATCTAGGGCGTGTGGCGGGTGG	5630
Qy	4982	CTGCTGAGGAGTACCTGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGATCA	5041
Db	5631	CTGCTGAGGAGTACCTGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGATCA	5690
Qy	5042	CCACTGACAAAGTAAAGTGCCTGTGAGTTCGGGCCCCCAATTTCTTCAGAGTGG	5101
Db	5691	CCACTGACAAAGTAAAGTGCCTGTGAGTTCGGGCCCCCAATTTCTTCAGAGTGG	5750
Qy	5102	ATGGGGTGGGTTGACAGGTACGCTCCAGCTGCAAAACCCCTCTACCGGGAGGATCA	5161
Db	5751	ATGGGGTGGGTTGACAGGTACGCTCCAGCTGCAAAACCCCTCTACCGGGAGGATCA	5810
Qy	5162	CATTCTGCTGGGCTCAATCAATACCTGGTTGGGTCAAGCTCCCATCGGAGCCCCGAAC	5221
Db	5811	CATTCTGCTGGGCTCAATCAATACCTGGTTGGGTCAAGCTCCCATCGGAGCCCCGAAC	5870
Qy	5222	CGGACGTAGAGTGTCACTTCATGCTACCGACCCCTCCACATTTACGGCGGAGACGG	5281
Db	5871	CGGACGTAGAGTGTCACTTCATGCTACCGACCCCTCCACATTTACGGCGGAGACGG	5930
Qy	5282	CTAAGCGTAGGCTGGCCAGGGATCTCCGCCCTCTGGGCGAGCTCATAGCTAGCCAGC	5341
Db	5931	CTAAGCGTAGGCTGGCCAGGGATCTCCGCCCTCTGGGCGAGCTCATAGCTAGCCAGC	5990
Qy	5342	TGCTGCGCTTCTTGAAGGCAACATGCACTACCCGTCATGATCTCCCGGACGCTGACC	5401
Db	5991	TGCTGCGCTTCTTGAAGGCAACATGCACTACCCGTCATGATCTCCCGGAGCCTGACC	6050
Qy	5402	TCATCGAGGCAACCTCTGTGGCGGAGGATGAGGGGGAACATCACCCGCTGGAGT	5461
Db	6051	TCATCGAGGCAACCTCTGTGGCGGAGGATGAGGGGGAACATCACCCGCTGGAGT	6110
Qy	5462	CAGAAATAGGTAGTAAATTTTGACTCTTTTCGAGCCGCTCCAAAGCGGAGGATGAGA	5521
Db	6111	CAGAAATAGGTAGTAAATTTTGACTCTTTTCGAGCCGCTCCAAAGCGGAGGATGAGA	6170
Qy	5522	GGGAGATTCCTGTTCCGGCGGAGATCTTCGGAGGTCCAGAAATTCCTCGAGCGATGC	5581
Db	6171	GGGAGATTCCTGTTCCGGCGGAGATCTTCGGAGGTCCAGAAATTCCTCGAGCGATGC	6230
Qy	5582	CCATATGGGACGCCGGATTAACACCTCCACTCTTAGGTCCTGGAAGGACCCGGACT	5641
Db	6231	CCATATGGGACGCCCGGATTAACACCTCCACTCTTAGGTCCTGGAAGGACCCGGACT	6290
Qy	5642	AGTCCCTCCAGTGTGACAGGGTGTCCATTGCCGCTGCCAAGGCCCTCCGATACCAAC	5701
Db	6291	AGTCCCTCCAGTGTGACAGGGTGTCCATTGCCGCTGCCAAGGCCCTCCGATACCAAC	6350
Qy	5702	CTCCAGGAGGAGGACGGTGTCTCTGATCTCAAGTCTACCGTGTCTTCTGCTTGGCGG	5761
Db	6351	CTCCAGGAGGAGGACGGTGTCTCTGATCTCAAGTCTACCGTGTCTTCTGCTTGGCGG	6410
Qy	5762	AGTCCGCAAAAGACTTTCGGCAGCTCCGAAATCTGTCGCGCTGCGACAGCGGCAAA	5821
Db	6411	AGTCCGCAAAAGACTTTCGGCAGCTCCGAAATCTGTCGCGCTGCGACAGCGGCAAA	6470
Qy	5822	CGGCTCTCTGACACAGCCCTCCGACGAGCGGCGACCGGGATCCGAGCTGCTGACT	5881
Db	6471	CGGCTCTCTGACACAGCCCTCCGACGAGCGGCGACCGGGATCCGAGCTGCTGACT	6530
Qy	5882	CCTCCATGCCCCCTTGAAGGGAGCGGGGATCCCGATCTCAGCGAGGGTCTTGGT	5941
Db	6531	CCTCCATGCCCCCTTGAAGGGAGCGGGGATCCCGATCTCAGCGAGGGTCTTGGT	6590
Qy	5942	CTACCGTGAAGGAGGCTAGTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6001
Db	6591	CTACCGTGAAGGAGGCTAGTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6650
Qy	6002	CAGGCGCTGATCAAGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGACTGA	6061
Db	6651	CAGGCGCTGATCAAGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGACTGA	6710
Qy	6062	GCAACTCTTTGCTCGTCAACAACCTTGGTCTATGCTACAACTCTCGCAGCGCAAGCC	6121
Db	6711	GCAACTCTTTGCTCGTCAACAACCTTGGTCTATGCTACAACTCTCGCAGCGCAAGCC	6770
Qy	6122	TGCGGCAAGAGTCACTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGGAGC	6181
Db	6771	TGCGGCAAGAGTCACTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGGAGC	6830
Qy	6182	TGCTCAAGAGATGAAGCGAAAGGCTCCACAGTTAAAGCTAAACTTCTATCGTGGAGG	6241
Db	6831	TGCTCAAGAGATGAAGCGAAAGGCTCCACAGTTAAAGCTAAACTTCTATCGTGGAGG	6890
Qy	6242	AAGCCTGTAAAGTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	6301
Db	6891	AAGCCTGTAAAGTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	6950
Qy	6302	AGCTCCGGAACCTATCCAGCAAGCGGCTTAAACACATCCGCTCCGTGTGGAAGACTTGC	6361
Db	6951	AGCTCCGGAACCTATCCAGCAAGCGGCTTAAACACATCCGCTCCGTGTGGAAGACTTGC	7010
Qy	6362	TGGAAGACTGAGACACCAATTTGACACCACTCATGGCAAAATGAGTTTCTGCG	6421
Db	7011	TGGAAGACTGAGACACCAATTTGACACCACTCATGGCAAAATGAGTTTCTGCG	7070
Qy	6422	TTGCTGTGTCGGAATAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCCGTGA	6481
Db	7071	TTGCTGTGTCGGAATAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCCGTGA	7130
Qy	6482	TGCGCTCTTTCATACGGAATCCAAATCTCTCTGACAGCGGCTGAGTTCTGTTGAAATG	6541
Db	7131	TGCGCTCTTTCATACGGAATCCAAATCTCTCTGACAGCGGCTGAGTTCTGTTGAAATG	7190
Qy	6542	TGCGCTCTTTCATACGGAATCCAAATCTCTCTGACAGCGGCTGAGTTCTGTTGAAATG	6601
Db	7191	TGCGCTCTTTCATACGGAATCCAAATCTCTCTGACAGCGGCTGAGTTCTGTTGAAATG	7250
Qy	6602	CCTGGAAGCGAAGAAATGCGCTTATGGCTTCGCAATGACACCGCTGTTTGACTCAA	6661
Db	7251	CCTGGAAGCGAAGAAATGCGCTTATGGCTTCGCAATGACACCGCTGTTTGACTCAA	7310
Qy	6662	CGCTCAGTGAAGTGAATCCGCTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGGCC	6721
Db	7311	CGCTCAGTGAAGTGAATCCGCTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGGCC	7370
Qy	6722	CGGAAGCGACAGCGCCATTAAGTTCGCTCAAGAGCGGCTTTACATCGGGGCCCCCTGA	6781
Db	7371	CGGAAGCGACAGCGCCATTAAGTTCGCTCAAGAGCGGCTTTACATCGGGGCCCCCTGA	7430
Qy	6782	CTAATTTTAAAGGGCAGAACTCGGCTATCGCGGTGCGCGCGAGCGGTGTACTGACGA	6841
Db	7431	CTAATTTTAAAGGGCAGAACTCGGCTATCGCGGTGCGCGCGAGCGGTGTACTGACGA	7490
Qy	6842	CCAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCGGCTCGGCTCTCGAGCTGCGA	6901
Db	7491	CCAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCGGCTCGGCTCTCGAGCTGCGA	7550
Qy	6902	AGCTCCAGACTGCAAGTGTCTGATGCGGAGACCACTTGTGTTTCTGTTGAAAGCG	6961
Db	7551	AGCTCCAGACTGCAAGTGTCTGATGCGGAGACCACTTGTGTTTCTGTTGAAAGCG	7610
Qy	6962	CGGGGACCCAGAGGAGGAGCGGCTACCGGCTTTCAGGAGGCTATGACTAGTACT	7021
Db	7611	CGGGGACCCAGAGGAGGAGCGGCTACCGGCTTTCAGGAGGCTATGACTAGTACT	7670
Qy	7022	CTGCCCCCTCTGGGACCCGCCAAACCAAGTGAAGTGTGATTAACATCATGCT	7081
Db	7671	CTGCCCCCTCTGGGACCCGCCAAACCAAGTGAAGTGTGATTAACATCATGCT	7730
Qy	7082	CTTCCAAATGTGTCAGTCCGCAAGTGTGCAAAAGGGTGTACTATCTCACCCGCTG	7141
Db	7731	CTTCCAAATGTGTCAGTCCGCAAGTGTGCAAAAGGGTGTACTATCTCACCCGCTG	7790

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QY 7142 ACCCACACCCCTTTCGGGGGCTGGTGGGAGACAGCTAGACACACTCCAGTCAATT 7201
DB 7791 ACCCACACCCCTTTCGGGGGCTGGTGGGAGACAGCTAGACACACTCCAGTCAATT 7850
QY 7202 CTTGGCTAGGCAACATCATCATGATGATCGGCCCACTTGTGGGCAAGATGATCTGTATGA 7261
DB 7851 CTTGGCTAGGCAACATCATCATGATGATGATCGGCCCACTTGTGGGCAAGATGATCTGTATGA 7910
QY 7262 CTCATTTCTTCTCATTCCTTCTAGCTCAGGAACAACCTTGAAAAAGCCCTAGATTGTTCAGA 7321
DB 7911 CTCATTTCTTCTCATTCCTTCTAGCTCAGGAACAACCTTGAAAAAGCCCTAGATTGTTCAGA 7970
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DB 7971 TCTACGGGGGCTGTACTCTCATTTAGCCACTTGACCTTACCTCAGATCATTCACAGACTCC 8030
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DB 8031 ACGGCCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTAGATCAATAGGGTGGCTT 8090
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DB 8631 TGCAGATCAAGT 8642
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RESULT 13

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US-10-029-907-6
; Sequence 6, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
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; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)... (8407)
; US-10-029-907-6
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Query Match 90.7%; Score 7245.6; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7958; Conservative 0; Mismatches 19; Indels 671; Gaps 3;
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QY 842 TGTGATCAGATGATCTGGAGCAAGAGCATACGGGGCTCGCGCCAGCGCAACTGTTCGC 901
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Qy	902	CAGGCTCAAGGCGGCATGCGCGAGGAGATCTCGTGTGACCCATGCGGATGCGCTG	961	1804	-----	1803
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Qy	962	CTTGCCGAATATCATGCTGGAATATGCGCGCTTTCTGATTCATCGACTGTGGCGGCT	1021	1804	-----	1803
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Qy	1142	GCGCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGATTT-----TAAAC	1189	1804	-----	1803
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Qy	1250	ACGTTACTGCGGAGCGCTTGGAATAAGCCGCTGCGTTGTCTATATGTTATTTT	1310	1804	-----	1803
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Qy	1310	CCACCATATTTGCCGTTTGGCAATGTAGGGCCCGGAACCTGCGCCTCTCTCTTGA	1369	1804	-----	1803
Db	1310	CCACCATATTTGCCGTTTGGCAATGTAGGGCCCGGAACCTGCGCCTCTCTCTTGA	1369	2391	GGGGAGGGAGATATCATCTGGGACCGGCAGACACCTTTGAAGSGCAGGGTGGCGACTCC	2450
Qy	1370	CGAGCATTTCTAGGGGTTTCCCTCTCGCAAGGAATGCAAGGCTCTGTTGAATGTCG	1429	1804	--GCGCCTATTAGGCGCTACTCCCAACAGACGCGAGGCGCTACTTTGGTGTGATCATCACTA	1861
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Db	1430	TGAAGGAGCAGTTCCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGAGGACCCCTT	1489	2511	GCCTCACAGGCGGGAAGGAAACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCAA	2570
Qy	1490	CGAGCAGCGGAACCCCGACCTGCGGACAGGTGCTCTGCGGCCAAGCAAGCTGTAT	1549	1922	CACATCTTTCTCGGCGACTGCGTCAATGCGGTGTGTGGACTGTCTATCATGTGCGG	1981
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Db	1550	AAGATACACCTGCAAAAGGCGGCACAAACCCAGTGCACGTTGTGAGTTGGATGTTGG	1610	2631	GCTCAAGACACCTTTGCCGCGCCCAAGGGCCCAATGCCAAATGTACACCAATGTGGACC	2690
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5391	TCCCTCTCTCTCAATGTAAGTGGGTACAAGGAGTCTGGCGGCGGACGATCATGCG	5450	6471	CGGCTCTCTTACAGAGCCCTCCGACGCGCGGATCCCGGATCCCGACGTTGAGTCTGACT	6530
4802	AAACCACTGCCATGTGGAGCACAGATCAACGGACATGTGAAAAACGGTTCCATGAGGA	4861	5882	CTTCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGT	5941
5451	AAACCACTGCCATGTGGAGCACAGATCAACGGACATGTGAAAAACGGTTCCATGAGGA	5510	6531	CTTCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGGATCCCGACGTTGAGTCTGACT	6590
4862	TGCTGGGGCTAGGACCTGTGTAAACAGTGGGATGGAACATTTCCCGATTAACCGGTACA	4921	5942	CTACCGTAAAGCGAGGAGGTAGTGGAGGAGTGGTGGTCTGCTGCTCGATGCTACACATGGA	6001
5511	TGCTGGGGCTAGGACCTGTGTAAACAGTGGGATGGAACATTTCCCGATTAACCGGTACA	5570	6591	CTACCGTAAAGCGAGGAGGTAGTGGAGGAGTGGTGGTCTGCTGCTCGATGCTACACATGGA	6650
4922	CCACGGGCCCTGCAACCCCTCCCGCGCGCAATTTCTAGGGGCTGTGGCGGGTGG	4981	6002	CAGGCGCCCTGATCAACCGATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGA	6061
5571	CCACGGGCCCTGCAACCCCTCCCGCGCGCAATTTCTAGGGGCTGTGGCGGGTGG	5630	6651	CAGGCGCCCTGATCAACCGATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGA	6710
4982	CTGCTGAGGAGTACGTGGAGGTACGCGGGTGGGGATTTCCACTAGCTGACGGGCATGA	5041	6062	GCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTAACAATCTCGAGCGCAGACC	6121
5631	CTGCTGAGGAGTACGTGGAGGTACGCGGGTGGGGATTTCCACTAGCTGACGGGCATGA	5690	6711	GCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTAACAATCTCGAGCGCAGACC	6770
5042	CACTGACAAAGTAAAGTCCCGTGTCAAGTTCGCGGCCCGGAATTTCTACAGAGTGG	5101	6122	TGCGGCAAGAAAGGTCACTTTGACAGACTGCGAGTCCCTGGAGCAGCACTTACCGGACG	6181
5691	CACTGACAAAGTAAAGTCCCGTGTCAAGTTCGCGGCCCGGAATTTCTACAGAGTGG	5750	6771	TGCGGCAAGAAAGGTCACTTTGACAGACTGCGAGTCCCTGGAGCAGCACTTACCGGACG	6830
5102	ATGGGGTGGCTTGCACAGGTACGCTCAGCGTGCAGCCCTCTCAGGGAGGAGTCA	5161	6182	TGCTCAAGGAGATGAAAGCGGAGCGGCTCCAGTTCAGAGGCTTAAATTTGGCTTAAAGCT	6241
5751	ATGGGGTGGCTTGCACAGGTACGCTCAGCGTGCAGCCCTCTCAGGGAGGAGTCA	5810	6831	TGCTCAAGGAGATGAAAGCGGAGCGGCTCCAGTTCAGAGGCTTAAATTTGGCTTAAAGCT	6890
5162	CATTCTGGCTCGGCTCAATCAATACCTGTTGGGTCAAGTCCCATGCGAGCCCGAAC	5221	6242	AAGCTGTGAGTGTGACGCCGCCCAATTCGCGGCGAGTCACTTAAATTTGGCTTAAAGCT	6301
5811	CATTCTGGCTCGGCTCAATCAATACCTGTTGGGTCAAGTCCCATGCGAGCCCGAAC	5870	6302	ACGTCCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTGTGGAGGACTTGC	6361
5222	CGGAGTACAGTGTCTATTCATGCTCAACGACCTTCCACATTAAGCGGAGAGCGG	5281	6951	ACGTCCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTGTGGAGGACTTGC	7010
5871	CGGAGTACAGTGTCTATTCATGCTCAACGACCTTCCACATTAAGCGGAGAGCGG	5930	6362	TGGAGACACTGAGACACCAATTCACACACCATCATGGCAAAATAAGGTTTCTGCG	6421
5282	CTAAGCGTAGGTGCGGAGGATCTCCCGCTCTGGCCAGCTCATCAGTAGCCAGC	5341	7011	TGGAGACACTGAGACACCAATTCACACACCATCATGGCAAAATAAGGTTTCTGCG	7070
5931	CTAAGCGTAGGTGCGGAGGATCTCCCGCTCTGGCCAGCTCATCAGTAGCCAGC	5990	6422	TCCAAACAGAGAGGGGGCGCAAGCAGCTGCGCTTATCGTATTCAGATTTGGGGG	6481
5342	TGCTCGGCTTCTCTTGAAGCAACATGACATACCCCTGCTGAGCTCCCGGACGCTGACC	5401	7071	TCCAAACAGAGAGGGGGCGCAAGCAGCTGCGCTTATCGTATTCAGATTTGGGGG	7130
5991	TGCTCGGCTTCTCTTGAAGCAACATGACATACCCCTGCTGAGCTCCCGGACGCTGACC	6050	6482	TTCTGTGTGCGAGAAATAGGCGCTTACGATGTGCTTCCACCTCCCTCAGGCGGTGA	6541
5402	TCATCGAGCCCAACTCTCTGCGGCGAGGATGGCGGGGACATCACCGCGTGGGT	5461	7131	TTCTGTGTGCGAGAAATAGGCGCTTACGATGTGCTTCCACCTCCCTCAGGCGGTGA	7190
6051	TCATCGAGCCCAACTCTCTGCGGCGAGGATGGCGGGGACATCACCGCGTGGGT	6110	6542	TGCGGCTCTTATACCGATTCCAATATCTCTCTGAGCAGCGGCTGAGGTTCTGCTGGAATG	6601
5462	CAGAAATAAGTGTATTTTGGACTCTTTCAGCGCTTCCAAAGCGGAGGAGATGAGA	5521	7191	TGCGGCTCTTATACCGATTCCAATATCTCTCTGAGCAGCGGCTGAGGTTCTGCTGGAATG	7250
6111	CAGAAATAAGTGTATTTTGGACTCTTTCAGCGCTTCCAAAGCGGAGGAGATGAGA	6170	6602	CCTGGAAGCGAAGAAATGCCCTATGGGCTTCGATATGACACCGCGCTGTTGACTCAA	6661
5522	GGAAGTATCCGTTCCGGGGGAGATCTCGGAGGTCCAGGAAATTCCTTCGAGCGATGC	5581	7251	CCTGGAAGCGAAGAAATGCCCTATGGGCTTCGATATGACACCGCGCTGTTGACTCAA	7310
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5582	CCATATGGGCAACCGCGGATTAACAACCTCCATGTTAGTCTGGAAGACCCGACT	5641	7311	CGGTCTAGAGATGACATCCGTTGAGGAGTCAATCTACCAATGTTGTGACTTGCCCC	7370
6231	CCATATGGGCAACCGCGGATTAACAACCTCCATGTTAGTCTGGAAGACCCGACT	6290	6722	CCGAAGCGAGAGGCGATTAAGGTGCTCAGAGCGGCTTTATCATCGGGGGCCCCCTGA	6781
5642	ACGTCCCTCCAGTGGTACAGGGTGTCCATTGCGCGCTGCAAGGCCCTCCGATACAC	5701	7371	CCGAAGCGAGAGGCGATTAAGGTGCTCAGAGCGGCTTTATCATCGGGGGCCCCCTGA	7430

[illegible]

QY	7862	TTTTCTCTTTTTTTTCCCTTTTCTTTTCCCTTGGTGGCTCCCATCTTAGCGCTAGTCA	CGGCT	7921
Db	8511	TTTTCTCTTTTTTTTCCCTTTTCTTTTCCCTTGGTGGCTCCCATCTTAGCGCTAGTCA	CGGCT	8570
QY	7922	AGCTGTGAAAGGTCCGTGAGCGCGCTTGACTGCACAGAGAGTGTGATAC	TGGCCTCTCTTGCA	7981
Db	8571	AGCTGTGAAAGGTCCGTGAGCGCGCTTGACTGCACAGAGAGTGTGATAC	TGGCCTCTCTTGCA	8630
QY	7982	GATCAAGT	7989	
Db	8631	GATCAAGT	8638	

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RESULT 14
US-10-029-907-5
; Sequence 5, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 8648
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802) ... (8407)
US-10-029-907-5

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Query Match 90.5%; Score 7229.8; DB 4; Length 8648;
Best Local Similarity 91.9%; Pred. No. 0;
March 27, 2001

[illegible]

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Db	481	CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGCGCCCGGTTCTTTTGTTCAGACCG	540	QY	1609	GAAAGAGTCAATGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATCCCGAGAG	1668
QY	541	ACCTGTCGGTCCCTGATGAACTGACGAGGCGAGCGGCTATCGTGGCTGGCCA	600	Db	1610	GAAAGTCAATGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATCCCGAGAG	1669
Db	541	ACCTGTCGGTCCCTGATGAACTGACGAGGCGAGCGGCTATCGTGGCTGGCCA	600	QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTAT	1728
QY	601	CGACGGGCTTCTTGGCGAGCTGTCTGACAGTGTCTACAGCGGGAAGGACTGCG	660	Db	1670	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTAT	1729
Db	601	CGACGGGCTTCTTGGCGAGCTGTCTGACAGTGTCTACAGCGGGAAGGACTGCG	660	QY	1729	TCAGGTTTAAAGAAAGTCTAGGCCCCCGAAACCAAGGGGACGTGTTTCTTTGAAAA	1788
QY	661	TGCTATTGGCGGAAGTCCCGGGCAGGATCTCTGTCTCATCTCACCTTGTCTCGCGAGA	720	Db	1730	TCAGGTTTAAAGAAAGTCTAGGCCCCCGAAACCAAGGGGACGTGTTTCTTTGAAAA	1789
Db	661	TGCTATTGGCGGAAGTCCCGGGCAGGATCTCTGTCTCATCTCACCTTGTCTCGCGAGA	720	QY	1789	CACGATAATACCATG-----	1803
QY	721	AGATATCCATCATGGCTGATGCAATGGCGGCTGCATACGCTTGATTCGGCTACCTGCC	780	Db	1790	CACGATAATACCATGACCGGGAGATGGCAGCATCTGTCGGAGCGCGTTCCTGTTAGT	1849
Db	721	AGATATCCATCATGGCTGATGCAATGGCGGCTGCATACGCTTGATTCGGCTACCTGCC	780	QY	1804	-----	1803
QY	781	CATTGACACCAAGCGAAACATCGCATCGAGCGAGCACCTACTCGGATCGAAGCGCGTC	840	Db	1850	CTGATACTCTTGACCTTGTACCGCACTATAAGCTGTTCTCGTAGGCTCATATGTTG	1909
Db	781	CATTGACACCAAGCGAAACATCGCATCGAGCGAGCACCTACTCGGATCGAAGCGCGTC	840	QY	1804	-----	1803
QY	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGGCCAGCGCACTGTTCG	900	Db	1910	TTACAATATTTTATACAGGGCGGAGGACACATTGCAAGTGTGATCCCGCCCTCAAC	1969
Db	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGGCCAGCGCACTGTTCG	900	QY	1804	-----	1803
QY	901	CCAGGCTCAAGCGCGCATGCCGACCGGAGGATCTGCTGACACCATGGCCATGCT	960	Db	1970	GTTCGGGGGGCGCGATGCCGTCATCTCTCACGTGCGCATCCACCCAGAGCTAATC	2029
Db	901	CCAGGCTCAAGCGCGCATGCCGACCGGAGGATCTGCTGACACCATGGCCATGCT	960	QY	1804	-----	1803
QY	961	GCTTGGCGGAATCATGTGGAATAGCCGCTTTCTTGGATTCATGACACTGTGGCGGC	1020	Db	2030	TTTACCATCACCAAAATCTTGTCTGCCATACTCGGTCCACTCATGTGCTCCAGGCTGT	2089
Db	961	GCTTGGCGGAATCATGTGGAATAGCCGCTTTCTTGGATTCATGACACTGTGGCGGC	1020	QY	1804	-----	1803
QY	1021	TGGGTGTGGCGGACCGCTATCAGGATAGCGTTGGCTACCGTGATTTCTGAGAGC	1080	Db	2090	ATAACCAAGTGCCTACTTCTGGCGGCACACAGGGCTCATTCGTGATGATGCTGTG	2149
Db	1021	TGGGTGTGGCGGACCGCTATCAGGATAGCGTTGGCTACCGTGATTTCTGAGAGC	1080	QY	1804	-----	1803
QY	1081	TGGCGGGGAATGGGCTGACCGCTTCTGCTGCTTTACGGTATCCCGCTCCCGATTCGC	1140	Db	2150	CGAAGTTGTGGGGTCAATTAATGTCACCAATGGCTCTCATGAAGTTGGCGCACTGACA	2209
Db	1081	TGGCGGGGAATGGGCTGACCGCTTCTGCTGCTTTACGGTATCCCGCTCCCGATTCGC	1140	QY	1804	-----	1803
QY	1141	AGCGATCGCTTCTATCGCTTCTTACAGATTTCTTGAATTTCTTGAATTTCTTGAAT	1200	Db	2210	GGTACGTACGTTTATGACCATCTCACCCACTGCGGAGCTGGGCCACCGCGGCTACGA	2269
Db	1141	AGCGATCGCTTCTATCGCTTCTTACAGATTTCTTGAATTTCTTGAATTTCTTGAAT	1200	QY	1804	-----	1803
QY	1189	CAGACCAACCGTTTCCCTTAGCGGGATCAATTCGGCCCTCTCCCTCCCCCCCCCT	1248	Db	2270	GACCTTGGCGGTGGGATTTGAGCCCGTCTTCTCTGATATGAGACCAAGGTTATCACC	2329
Db	1189	CAGACCAACCGTTTCCCTTAGCGGGATCAATTCGGCCCTCTCCCTCCCCCCCCCT	1248	QY	1804	-----	1803
QY	1249	AAGTTTACGCGAGCGCTTGGAAATAGGCGGCTGTGCGTTTGTCTATATGTTATTT	1308	Db	2330	TGGGGGCGAGACACCGCGCGTGTGGGACATCATCTTGGGCTGCGGCTCCCGCCCGC	2389
Db	1249	AAGTTTACGCGAGCGCTTGGAAATAGGCGGCTGTGCGTTTGTCTATATGTTATTT	1308	QY	1804	-----	1803
QY	1309	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTCTTG	1368	Db	2390	AGGGGAGGAGATACATCTGGACCGGACAGAGCTTTGAAGGCGAGGGTGGCGACTC	2449
Db	1309	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTCTTG	1368	QY	1804	-----	1803
QY	1369	ACGAGCATCTAGGGGTCTTTCCCTCTCGCAAGAGGATGCAAGTCTGTTGAATGTC	1428	Db	2450	CTCGCGCTTATAGGCTTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT	2509
Db	1369	ACGAGCATCTAGGGGTCTTTCCCTCTCGCAAGAGGATGCAAGTCTGTTGAATGTC	1428	QY	1861	AGCCTCACAGGCGGACAGGAACAGGTCGAGGGGAGTCCAGTGTCTCCACCGCA	1920
QY	1429	GTGAGGAAGCAGTCTCTGGAAGCTTCTTGAAGACAAACAAAGCTGTAGGACCCCT	1488	Db	2510	AGCCTCACAGGCGGACAGGAACAGGTCGAGGGGAGTCCAGTGTCTCCACCGCA	2569
Db	1429	GTGAGGAAGCAGTCTCTGGAAGCTTCTTGAAGACAAACAAAGCTGTAGGACCCCT	1488	QY	1921	ACAAATCTTCTCGGACCTCGTCAATGGCGTGTGTTGGAAGTCTCTATCATGTGTC	1980
QY	1489	TGACGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGGCAAAAGCCACGTGA	1548	Db	2570	ACAAATCTTCTCGGCGACCTCGTCAATGGCGTGTGTTGGAAGTCTCTATCATGTGTC	2629
Db	1489	TGACGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGGCAAAAGCCACGTGA	1548	QY	1981	GGTCAAGACCTTTCGCGGCCCAAGGGGCCAATCAACCAATGTATCAACATGTGAC	2040
QY	1549	TAAGATACACCTGCAAGGGCGGCAACCCAGTGTGTTGATGATGTTG	1608				

Db	2630	GGCTCAAAGACCCCTTGC	CGGCCCAAAAGGCCCAATCACCCAAATGTACACCAATGTGCAC	2689
QY	2041	CAGGACCTCGTCCGGCTGGCAAGCCGCCCGGGCGGTTCTTTGACACCAATGACACTGC	2100	
Db	2690	CAGGACCTCGTCCGGCTGGCAAGCCGCCCGGGCGGTTCTTTGACACCAATGACACTGC	2749	
QY	2101	GGCAGCTCGGACCTTTACTTTGGTTCAGAGSCATGCCGATGCTCATTC	CGGGTGC	2160
Db	2750	GGCAGCTCGGACCTTTACTTTGGTTCAGAGGCAATCCGATGTCTATTC	CGGGTGC	2809
QY	2161	GGCGACAGCAGGGGAGCTACTCTCCCAAGCCCGTCTCTTACTTTGAAGGGCTCTTCG	2220	
Db	2810	GGCGACAGCAGGGGAGCTACTCTCCCAAGCCCGTCTCTTACTTTGAAGGGCTCTTCG	2869	
QY	2221	GGCGTCCACTCTCTGCCCCCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCGGTGTGC	2280	
Db	2870	GGCGTCCACTCTCTGCCCCCTCGGGGACGCTGTGGGCATCTTTTCGGGCTGCGGTGTGC	2929	
QY	2281	ACCCGAGGGTTGGAAGGCGGTGGACTTTGTATCCCGTCCGAGTCTATGTGAAACCACTATG	2340	
Db	2930	ACCCGAGGGTTGGAAGGCGGTGGACTTTGTATCCCGTCCGAGTCTATGTGAAACCACTATG	2989	
QY	2341	CGGTCCCGGHTTTCACGGAACAATCGTCCCTCTCGGCCGTAACCGCAGACATTCCAGGTG	2400	
Db	2990	CGGTCCCGGHTTTCACGGAACAATCGTCCCTCTCGGCCGTAACCGCAGACATTCCAGGTG	3049	
QY	2401	GCCCATCTACAGCCCCCTACTGGTAGCGGCAAGACACTTAAGGTGCGGGCTCGGTATGCA	2460	
Db	3050	GCCCATCTACAGCCCCCTACTGGTAGCGGCAAGACACTTAAGGTGCGGGCTCGGTATGCA	3109	
QY	2461	GCCCAAGGGTATAGGTGCTTGTGCTGAAACCGTCCGTCGCCGCCACCTAGGTTTCGGG	2520	
Db	3110	GCCCAAGGGTATAGGTGCTTGTGCTGAAACCGTCCGTCGCCGCCACCTAGGTTTCGGG	3169	
QY	2521	GGGTATATGCTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGGTAAGGACCATC	2580	
Db	3170	GGGTATATGCTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGGTAAGGACCATC	3229	
QY	2581	ACCACGGGTCCCCCATCAAGTACTCCACCTATGCGAAGTTTCTTCCGACGGTGGTTGC	2640	
Db	3230	ACCACGGGTCCCCCATCAAGTACTCCACCTATGCGAAGTTTCTTCCGACGGTGGTTGC	3289	
QY	2641	TCGTGGGGCGCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700	
Db	3290	TCGTGGGGCGCTATGACATCATTAATATGTGATGAGTGCACCTCAACTGACTCGACCACT	3349	
QY	2701	ATCCTGGGATCGGACAGTCCCTGGCAACCGGAGACGGCTGGAGCGGACTCGTGGT	2760	
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QY	2761	CTCGCCACCGCTACGCTCCGGATCGGTCAACGTCACATCCAAACATCGAGAGGTG	2820	
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QY	2821	GCTGTGTCAGACATGGAGAAATCCCTTTATGGCAAGCCATCCCCATCGAGACCATC	2880	
Db	3470	GCTGTGTCAGACATGGAGAAATCCCTTTATGGCAAGCCATCCCCATCGAGACCATC	3529	
QY	2881	AAGGGGGGAGGACCTCTATTTCTGCCATTCCAAGAGAAATGTGATGAGTGC	2940	
Db	3530	AAGGGGGGAGGACCTCTATTTCTGCCATTCCAAGAGAAATGTGATGAGTGC	3589	
QY	2941	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACCGGGCCCTTGATGTATCCGTC	3000	
Db	3590	AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACCGGGCCCTTGATGTATCCGTC	3649	
QY	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACCGGACGCTCTAATGAGGGCTTTACC	3060	
Db	3650	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACCGGACGCTCTAATGAGGGCTTTACC	3709	
QY	3061	GGCGATTTTCGACTCAGTGTGATCGACTGCATATCATGTGTACCCAGACAGTGCATTCAGC	3120	
Db	3710	GGCGATTTTCGACTCAGTGTGATCGACTGCATATCATGTGTACCCAGACAGTGCATTCAGC	3769	


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RESULT 15

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US-10-029-907-4
; Sequence 4, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8643
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)....(8407)
US-10-029-907-4
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Query Match 90.4%; Score 7222.6; DB 4; Length 8643;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 7953; Conservative 0; Mismatches 24; Indels 676; Gaps 4;
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QY 2 CCAGCCCCCGATTGGGGGAGACACTCCACATAGATCACTCCCTCTGTAGGAACTACTGT 61
Db 2 CCAGCCCCCGATTGGGGGAGACACTCCACATAGATCACTCCCTCTGTAGGAACTACTGT 61
QY 62 CTTTCAGCAGAAAGCGCTTAGCCATGCGCTTAGTATGATGCTGTGAGCCTCCAGAAC 121
Db 62 CTTTCAGCAGAAAGCGCTTAGCCATGCGCTTAGTATGATGCTGTGAGCCTCCAGAAC 121
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QY	122	CCCCCTCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTTGCCAGG	181	QY	1190	AGACCACAAACGGTTTCCCTCTAGCGGGATCAATTCGGCCCTCTCCCTCCCCCCCCCCTA	1249
Db	122			Db	1202	AGACCACAAACGGTTTCCCTCTAGCGGGATCAATTCG	1250
QY	122	CCCCCTCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTTGCCAGG	181	QY	1250	AGTTTACTGGCCGGAAGCGCTTGGAAATAAGCGCGGTGCGTTTGTCTATATGTTATTTT	1309
Db	182	ACGACCGGTCTCTTCTTGATCAACCCCGCTCAATGCTTGGAGATTTGGCGGTGCCCGG	241	Db	1251	ACGTTTACTGGCCGGAAGCGCTTGGAAATAAGCGCGGTGCGTTTGTCTATATGTTATTTT	1310
QY	182	ACGACCGGTCTCTTCTTGATCAACCCCGCTCAATGCTTGGAGATTTGGCGGTGCCCGG	241	QY	1310	CAACCATATTTGCGGTCTTTTGGCAATGTGAGGGCCCGGAAAACCTGGCCCTGTCTCTGA	1369
Db	242	CGAGACTGCTAGCCGAGTGTGTTGGTTCGGAAGAGCCCTTGTGTACTGCTCTGATAGGG	301	Db	1311	CAACCATATTTGCGGTCTTTTGGCAATGTGAGGGCCCGGAAAACCTGGCCCTGTCTCTGA	1370
QY	242	CGAGACTGCTAGCCGAGTGTGTTGGTTCGGAAGAGCCCTTGTGTACTGCTCTGATAGGG	301	QY	1370	CGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTTCAATGTCTG	1429
Db	302	TGCTTCGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATCCTTAACC	361	Db	1371	CGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTTCAATGTCTG	1430
QY	302	TGCTTCGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATCCTTAACC	361	QY	1430	TGAAGAAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAAACCTGTGTAGCGACCTTT	1489
Db	362	TCAAGAAAAACCAAGGGCGGCGCATGATTTGACAGATGATTTGACCGAGTTCCTCC	421	Db	1431	TGAAGAAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAAACCTGTGTAGCGACCTTT	1490
QY	362	TCAAGAAAAACCAAGGGCGGCGCATGATTTGACAGATGATTTGACCGAGTTCCTCC	421	QY	1490	GCAGGCAGCGGAACCCCCACCTGGGGAAGGTGCTCTCGGGCCAAAGCCAGCTGAT	1549
Db	422	GGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCACAAACAGCAATTCGGCTCTC	481	Db	1491	GCAGGCAGCGGAACCCCCACCTGGGGAAGGTGCTCTCGGGCCAAAGCCAGCTGAT	1550
QY	422	GGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCACAAACAGCAATTCGGCTCTC	481	QY	1550	AAGATACACCTGMAAGCGCGCACACCCAGTGCACGTTGTGAGTTGGATGTTGTGG	1609
Db	482	TGATGCGCGCTGTTCCGGCTGTGAGCGCAGGGCGCGCGGTCTCTTTTGTCAAGACCGA	541	Db	1551	AAGATACACCTGMAAGCGCGCACACCCAGTGCACGTTGTGAGTTGGATGTTGTGG	1610
QY	482	TGATGCGCGCTGTTCCGGCTGTGAGCGCAGGGCGCGCGGTCTCTTTTGTCAAGACCGA	541	QY	1610	AAAGAGTCAATGCTCTCTCAAGCGTATTCAACAGGGGCTGAAAGGATGCCAGAGG	1669
Db	542	CCTGTCCGGTGCCTGAAATGAACTGCAGGACGAGCGCGGTCTCTGCTGGCTGGCCAC	601	Db	1611	AAAGAGTCAATGCTCTCTCAAGCGTATTCAACAGGGGCTGAAAGGATGCCAGAGG	1670
QY	542	CCTGTCCGGTGCCTGAAATGAACTGCAGGACGAGCGCGGTCTCTGCTGGCTGGCCAC	601	QY	1670	TACCCCATTTGATGGGATCTGATCTGGGGCTCTGGTGACATGCTTTACATGTTTGTAGT	1729
Db	602	GACGGCGTCTCTTCGCGAGCTGTCTCGAAGTGTCTACTAAGCGGAAAGGAGCTGCT	661	Db	1671	TACCCCATTTGATGGGATCTGATCTGGGGCTCTGGTGACATGCTTTACATGTTTGTAGT	1730
QY	602	GACGGCGTCTCTTCGCGAGCTGTCTCGAAGTGTCTACTAAGCGGAAAGGAGCTGCT	661	QY	1730	CGAGTTTAAAGAGTCTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTTGAAGAAC	1789
Db	662	GCTATTGGCGAAGTTCGCGGGGAGGATCTCTGTCTCATCTACCTTGTCTCTGGCGAGAA	721	Db	1731	CGAGTTTAAAGAGTCTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTTGAAGAAC	1790
QY	662	GCTATTGGCGAAGTTCGCGGGGAGGATCTCTGTCTCATCTACCTTGTCTCTGGCGAGAA	721	QY	1790	ACGATAATACCATG	1803
Db	722	AGTATCCATCATGGCTGATGATCGGCGGTGATACGCTTGTGATCGGGTACCTTGCC	781	Db	1791	ACGATAATACCATG	1850
QY	722	AGTATCCATCATGGCTGATGATCGGCGGTGATACGCTTGTGATCGGGTACCTTGCC	781	QY	1804	-----	1803
Db	782	ATTTCGACCAAGCAACATCGCATCGAGCGAGCACCTACTCGGATGGAAGCGGTCT	841	Db	1851	TCGATCTCTTGACCTTGTACCGCACATATAAGCTGTTCCTCGTAGGCTCATATGTTGT	1910
QY	782	ATTTCGACCAAGCAACATCGCATCGAGCGAGCACCTACTCGGATGGAAGCGGTCT	841	QY	1804	-----	1803
Db	842	TGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCAGCGGACGTGTCG	901	Db	1911	TACAAATATTTATCACAGGGCGGAGGACACATTGCAAGTGTGATCCCCCCTCAACG	1970
QY	842	TGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCAGCGGACGTGTCG	901	QY	1804	-----	1803
Db	902	CAGGCTCAAGCGCGCATGCGCCAGCGAGGATCTGTCGTCGACCCATGGCCATGCTG	961	Db	1971	TTCCGGGGGCGCGGATGCGTCTCCTCTCACGTGCGGATCCACCCAGAGCTAATCT	2030
QY	902	CAGGCTCAAGCGCGCATGCGCCAGCGAGGATCTGTCGTCGACCCATGGCCATGCTG	961	QY	1804	-----	1803
Db	962	CTTTCGCAATATCATGTGTGGAATAATGGCCCTTTTCTGGAATCATGCACTGTGGCGGCT	1021	Db	2031	TTACCATCACCAAAATCTTGTCTGCCATCTCGGTCCACTCATGTGGTCTCCAGGCTGGA	2090
QY	962	CTTTCGCAATATCATGTGTGGAATAATGGCCCTTTTCTGGAATCATGCACTGTGGCGGCT	1021	QY	1804	-----	1803
Db	1022	GGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATATTGCTGAGAGCT	1081	Db	2091	TAAACAAAGTGCCTACTTCGTGGCGCACACGGGCTCATTCGTGCATGCTGTGTGTC	2150
QY	1022	GGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATATTGCTGAGAGCT	1081	QY	1804	-----	1803
Db	1082	TGGCGGCAATGGCTGACCCCTTCTGCTGCTTTTACGGTATCGCGCTCCCGATTCGCA	1141	Db	2151	GGAAGTTGCTGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCTACGACAG	2210
QY	1082	TGGCGGCAATGGCTGACCCCTTCTGCTGCTTTTACGGTATCGCGCTCCCGATTCGCA	1141	QY	1804	-----	1803
Db	1142	GCGCATCGCCCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTT-----TAAAC	1189	Db	2211	GTACGTAGTTTATGACCATCTACCCACATGCGGGGACTGGGCCACGCGGGCCTACGAG	2270
QY	1142	GCGCATCGCCCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTT-----TAAAC	1201	QY	1804	-----	1803

Db	2271	ACCTTGGCGTGGCAGTTGAGCCCGTCTGTCCTCTCTGATATGGAGACCAAGGTTATCACCT	2333
Qy	1804	-----	1803
Db	2331	GGGGGGCAGACACCGCGGCGTGTGGGACATCATCTTGGGCGCTGCCCGTCTCCGCCGCA	2390
Qy	1804	-----	1803
Db	2391	GGGGGAGGAGATACATCTGGGACCGGCAGACAGCCTTGAAGGCGAGGGGTGGCGACTCC	2450
Qy	1804	--GCCCTATTAGGCGCTACTCCCAACAGACGCGAGCCCTACTTGGCTGCATCATCACATA	1861
Db	2451	TGCGCCCTATTACGCGCTACTCCCAACAGACGCGAGCCCTACTTGGCTGCATCATCACATA	2510
Qy	1862	GCCTCACAGGCGGACAGGAACAGGTTCAGGGGAGGTCCAAGTGTCTCCACGCAA	1921
Db	2511	GCCTCACAGGCGGACAGGAACAGGTTCAGGGGAGGTCCAAGTGTCTCCACGCAA	2570
Qy	1922	CACAATCTTCTGTGCGACCTGCGTCAATGGCGTGTGTGGACTCTCTATCATGTGTCCG	1981
Db	2571	CACAATCTTCTGTGCGACCTGCGTCAATGGCGTGTGTGGACTCTCTATCATGTGTCCG	2630
Qy	1982	GCTCAAGACCTTGC CGGCGCAAGGCGCCAATCACCCAAATGACACCAATGTGGACC	2041
Db	2631	GCTCAAGACCTTGC CGGCGCAAGGCGCCAATCACCCAAATGTACCAATGTGGACC	2690
Qy	2042	AGGACCTCGTCGGCTGGCAGGCGCCCGGGGCGGTTCTTGCACCATGCACTGCG	2101
Db	2691	AGGACCTCGTCGGCTGGCAGGCGCCCGGGGCGGTTCTTGCACCATGCACTGCG	2750
Qy	2102	GCAGCTCGGACCTTTACTTGTGTACAGGAGATGCCGATGTCATTCGGTGGCGCGGGG	2161
Db	2751	GCAGCTCGGACCTTTACTTGTGTACAGGAGATGCCGATGTCATTCGGTGGCGCGGGG	2810
Qy	2162	GCAGACGAGGGGAGCTACTCTCCCGCAGGCGCGTCTCTACTCTGAAGGCTCTTCGG	2221
Db	2811	GCAGACGAGGGGAGCTACTCTCCCGCAGGCGCGTCTCTACTCTGAAGGCTCTTCGG	2870
Qy	2222	GCGGTCCACTGCTCTGCCCTTCGGGCAACGCTGTGGGCATCTTTTCGGGCTGCCGTGCA	2281
Db	2871	GCGGTCCACTGCTCTGCCCTTCGGGCAACGCTGTGGGCATCTTTTCGGGCTGCCGTGCA	2930
Qy	2282	CCGAGGGGTTGCGAAGGGCGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATGC	2341
Db	2931	CCGAGGGGTTGCGAAGGGCGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATGC	2990
Qy	2342	GGTCCCGGTCTTTCAGGCAACTCGTCCCTCCGCGCGTACCGCAGACATCCAGGTG	2401
Db	2991	GGTCCCGGTCTTTCAGGCAACTCGTCCCTCCGCGCGTACCGCAGACATCCAGGTG	3050
Qy	2402	CCATCTACAGCCCTACTGTAGGGCAAGCACTAAGTGC CGGCTGCGTATGCGAG	2461
Db	3051	CCATCTACAGCCCTACTGTAGGGCAAGCACTAAGTGC CGGCTGCGTATGCGAG	3110
Qy	2462	CCCAAGGTTAAGTGTCTTCCCTGAACCCGTCGTCGCGGCAACCTTAGGTTTCGGGG	2521
Db	3111	CCCAAGGTTAAGTGTCTTCCCTGAACCCGTCGTCGCGGCAACCTTAGGTTTCGGGG	3170
Qy	2522	CGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAAGCAATCA	2581
Db	3171	CGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAAGCAATCA	3230
Qy	2582	CCAGGGTGC C C C C A T C A G T A C T C C A A G T T T C T G C C A C G G T G T G C T	2641
Db	3231	CCAGGGTGC C C C C A T C A G T A C T C C A A G T T T C T G C C A C G G T G T G C T	3290
Qy	2642	CTGGGGCGCTATGACATCATATATGTATGTAGTGCCACTCAACTGACTCGACCACTA	2701
Db	3291	CTGGGGCGCTATGACATCATATATGTATGTAGTGCCACTCAACTGACTCGACCACTA	3350
Qy	2702	TCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGCGGCTGGAGCGGACTCTGCTGTC	2761

Db	3351	TCCTGGCCATCGGCACAGTCTTGGACCAAGCGAGACGGCTGGAGCGCGACTCGTGGTC	3411
QY	2762	TGCGCACCGCTAGCCTCCGGGATCGGTCAACGTGGCCACATCCAAACATCGAGGAGGTGG	2821
Db	3411	TGCGCACCGCTAGCCTCCGGGATCGGTCAACGTGGCCACATCCAAACATCGAGGAGGTGG	3470
QY	2822	CTCTGTCCAGCACTCGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACATCA	2881
Db	3471	CTCTGTCCAGCACTCGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACATCA	3530
QY	2882	AGGGGGGAGGACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCA	2941
Db	3531	AGGGGGGAGGACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCA	3590
QY	2942	AGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACCGGGCCCTTGATGATCCGTCA	3001
Db	3591	AGCTGTCCGGCTCGGACTCAATGCTGAGCATATTACCGGGCCCTTGATGATCCGTCA	3650
QY	3002	TACCACTAGCGGAGACGTCTATTGCTGAGCAACGAGCGCTCTAATGACGGCTTTACCG	3061
Db	3651	TACCACTAGCGGAGACGTCTATTGCTGAGCAACGAGCGCTCTAATGACGGCTTTACCG	3710
QY	3062	GCGATTTGCACTCAGTGTGACTGCAATACATGTGTCAACGACAGTTCGACTTCAGCC	3121
Db	3711	GCGATTTGCACTCAGTGTGACTGCAATACATGTGTCAACGACAGTTCGACTTCAGCC	3770
QY	3122	TGGAACCGACCTTCAACATTCGAGACGACCGGTGCCAACAAGACGCGGTGTCAAGCTCGC	3181
Db	3771	TGGAACCGACCTTCAACATTCGAGACGACCGGTGCCAACAAGACGCGGTGTCAAGCTCGC	3830
QY	3182	AGCGCGAGGACGACTGGTAGGGGAGGATGGGCAATTCACAGTTTGTGACTCCAGGAG	3241
Db	3831	AGCGCGAGGACGACTGGTAGGGGAGGATGGGCAATTCACAGTTTGTGACTCCAGGAG	3890
QY	3242	AACGGCCCTCGGCATGTTTCGATTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGTG	3301
Db	3891	AACGGCCCTCGGCATGTTTCGATTCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGTG	3950
QY	3302	CTTGGTACGAGCTCAGCCCGCGAGACCTCAGTTAGGTGCGGGCTTACTTAAACAC	3361
Db	3951	CTTGGTACGAGCTCAGCCCGCGAGACCTCAGTTAGGTGCGGGCTTACTTAAACAC	4010
QY	3362	CAGGGTTGCCGTCTGCGAGGACATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTCA	3421
Db	4011	CAGGGTTGCCGTCTGCGAGGACATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTCA	4070
QY	3422	CCACATAGACGCCCATTTCTTGCCACGACTAAGCAGGACGAGACAACTTCCCTTACC	3481
Db	4071	CCACATAGACGCCCATTTCTTGCCACGACTAAGCAGGACGAGACAACTTCCCTTACC	4130
QY	3482	TGGTAGCATACAGGCTACGGTTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACC	3541
Db	4131	TGGTAGCATACAGGCTACGGTTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACC	4190
QY	3542	AAATGTGGAAGTCTCATACGGCTTAAAGCTTAACGCTGACGCGGCCAACGCCCTGCTGT	3601
Db	4191	AAATGTGGAAGTCTCATACGGCTTAAAGCTTAACGCTGACGCGGCCAACGCCCTGCTGT	4250
QY	3602	ATAGGCTGGGAGCCGTTCCAAACGAGGTTACTTACCACACACCCCATTAACCAATATCA	3661
Db	4251	ATAGGCTGGGAGCCGTTCCAAACGAGGTTACTTACCACACACCCCATTAACCAATATCA	4310
QY	3662	TGGCATGATGTGCGCTGACCTGGAGTTCGTCAACGAGCACCTGGGTGCTGTGAGCGGAG	3721
Db	4311	TGGCATGATGTGCGCTGACCTGGAGTTCGTCAACGAGCACCTGGGTGCTGTGAGCGGAG	4370
QY	3722	TCCTAGCAGCTTCGGCCGCTATTGCCCTGACAAACGAGCAGTGGTTCATTGTGGCGAGGA	3781
Db	4371	TCCTAGCAGCTTCGGCCGCTATTGCCCTGACAAACGAGCAGTGGTTCATTGTGGCGAGGA	4430
QY	3782	TCACTTTGTCCGAAAGCCGCCATCATTCGCCACAGGAGTCTCTTACCGGAGTTTCG	3841
Db	4431	TCACTTTGTCCGAAAGCCGCCATCATTCGCCACAGGAGTCTCTTACCGGAGTTTCG	4490

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3902 AACAAATCAACAGAAAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGAGCGAGGCTG 3961
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5642 AGTCCCTCCAGTGTGACAGCGGTGTCATTTGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGG 5701
6291 AGTCCCTCCAGTGTGACAGCGGTGTCATTTGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGG 6350
5702 CTCACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5761
6351 CTCACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6410
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QY 6482 TTGCTGTGTGCGAGAAATGGCCCTTTTACGATGTGTCTCCACCTCCCTCAGCCCGTGA 6541
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QY 6662 CGGTCACTGAGAAATCACAATCCGCTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCC 6721
Db 7311 CGGTCACTGAGAAATCACAATCCGCTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCC 7370
QY 6722 CCGAAGCCAGACAGGCCATAGGTGCTTACAGAGCGGCTTTACATCGGGGGCCCCCTGA 6781
Db 7371 CCGAAGCCAGACAGGCCATAGGTGCTTACAGAGCGGCTTTACATCGGGGGCCCCCTGA 7430
QY 6782 CTAATTTCTAAAGGGAGAACTCGCGCTATCGCGGTGCGCGGAGCGGTGTACTGACGA 6841
Db 7431 CTAATTTCTAAAGGGAGAACTCGCGCTATCGCGGTGCGCGGAGCGGTGTACTGACGA 7490
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QY 6962 CGGGGACCCAGAGGAGAGCGAGCGGCTTACGGGCTTACGGAGGCTATGACTAGACT 7021
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QY 7022 CTGCCCCCTCTGGGACCGGCCCAACAGAAATACGACTTGGAGTTGATAACATCATGCT 7081
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Db 7731 CCTCCAAATGTGTGCTGCGGCAGATGATCTGGCAAAAGGGTGTACTATCTCACCCGTG 7790
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QY 7859 ---TTTTTCTCTTT 7916
Db 8511 TCTTTTTTCCCAATTT 8570
QY 7917 CGGCTAGCTGGAAGGTCGCTGAGCGCTTGAAGCTGAGAGAGTGTGATAGTGGCTCT 7976
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QY 7977 CTGAGATCAAGT 7989
Db 8631 CTGAGATCAAGT 8643

Search completed: November 2, 2004, 07:21:45
Job time : 676 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 16:41:32 ; Search time 14582 Seconds
(without alignments)
19971.632 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagccccgattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795.4	10.0	935	7	CK284786
2	794	9.9	804	7	CK291519
3	794	9.9	856	7	CK287297
4	794	9.9	910	7	CK287930
5	794	9.9	933	7	CK291799
6	794	9.9	936	7	CK256977
7	794	9.9	947	7	CK298208
8	794	9.9	954	7	CK283361
9	778.8	9.7	811	7	CK288185
10	587	7.3	878	7	CK288711
11	577.4	7.2	789	8	AQ361914
12	559.8	7.0	620	8	AQ398387
13	542.4	6.8	549	8	CK801630
14	514.8	6.4	561	8	AQ447874
15	508	6.4	509	8	AQ447775
16	505.4	6.3	637	8	AQ447230
17	503.8	6.3	592	8	AQ449162
18	499	6.2	499	8	AQ398880
19	496.4	6.2	498	8	AQ398730
20	477.4	6.0	586	7	CK801096
21	475.8	6.0	857	8	AQ875013
22	474.8	5.9	710	8	BH972732
23	469.8	5.9	473	8	AQ397768
24	468.8	5.9	594	8	AQ397253

ALIGNMENTS

RESULT 1
CK284786

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

C 25 465.2 5.8 850 8 AQ875052
C 26 463.4 5.8 798 8 AQ876139
C 27 458.8 5.7 482 1 AL449872
C 28 456.8 5.7 861 8 AQ875040
C 29 455.6 5.7 815 8 AQ876134
C 30 451.2 5.6 799 8 AQ876220
C 31 450 5.6 784 8 AQ876152
C 32 444.6 5.6 790 8 AQ875904
C 33 437.2 5.5 797 8 AQ876297
C 34 434.6 5.4 765 7 CK283362
C 35 426.8 5.3 804 8 AQ876080
C 36 422.8 5.3 759 7 CK298209
C 37 414.6 5.2 791 8 AQ876019
C 38 409.4 5.1 748 8 AQ501530
C 39 408 5.1 635 8 AQ447643
C 40 408 5.1 656 8 AQ447140
C 41 404 5.1 790 8 AQ875912
C 42 404 5.1 791 8 AQ876201
C 43 402.6 5.0 856 8 AQ875050
C 44 401.8 5.0 760 7 CK287931
C 45 398.8 5.0 722 6 CD641598

CK284786 935 bp mRNA linear EST 02-AUG-2004
EST747508 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5',
end mRNA sequence.

CK284786 GI:39858698

EST.

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 935)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskiewicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST747509

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>.

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1. .935

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMAQ41"

/tissue_type="abiotic and biotic stress-treated leaves,"

callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar amounts."

ORIGIN		Query Match		10.0%; Score 795.4; DB 7; Length 935;		Best Local Similarity		99.9%; Pred. No. 1.8e-174;		Matches 796; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	386	CATGATTGAACAAGATGATGACGACGAGTTCTCGGCGGTTCTGGGTGGAGAGCTATT	445								
Db	31	CATGATTGAACAAGATGATGACGACGAGTTCTCGGCGGTTCTGGGTGGAGAGCTATT	90								
QY	446	CGGCTATGATCGGACACACACACATCGGCTCTGATCGCGCTGTTCTCGGCTGTC	505								
Db	91	CGGCTATGATCGGACACACACACATCGGCTCTGATCGCGCTGTTCTCGGCTGTC	150								
QY	506	AGCGCAGGGCGCGCGTCTTTTGTCAAGACCGACCTGTGCGGTGCCCTGAATGAAT	565								
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Db	211	GCAGGACGAGGCGCGCTATGCTGTGGCTGCGACGACGCGGCTTCTTGGCAGCTGT	270								
QY	626	GCTCGACGTTGCTACGAGCGGAGGAGGACTGGCTGCTATTGGCGAAGTGGCGGGCA	685								
Db	271	GCTCGACGTTGCTACGAGCGGAGGAGGACTGGCTGCTATTGGCGAAGTGGCGGGCA	330								
QY	686	GGATCTCTGTCATCTCACTTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAAT	745								
Db	331	GGATCTCTGTCATCTCACTTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAAT	390								
QY	746	CGCGCGGCTGATACGCTTGTATCGGCTACTGCGGCTATCGACACCAAGCAATCG	805								
Db	391	CGCGCGGCTGATACGCTTGTATCGGCTACTGCGGCTATCGACACCAAGCAATCG	450								
QY	806	CATCGACGAGCAGTACTCGATGGAAGCGGCTTGTGCTGATCAGATGATCGACGA	865								
Db	451	CATCGACGAGCAGTACTCGATGGAAGCGGCTTGTGCTGATCAGATGATCGACGA	510								
QY	866	AGAGCATCAGGGCTCGCGGCGAGCGAACTGTTCCGCGAGGCTCAAGCGCGCATGCCGA	925								
Db	511	AGAGCATCAGGGCTCGCGGCGAGCGAACTGTTCCGCGAGGCTCAAGCGCGCATGCCGA	570								
QY	926	CGCGGAGGATCTGCTGTGACCGATCGGCTGCTGCGGCTATCATGTTGGGAA	985								
Db	571	CGCGGATGATCTGCTGCTGACCCATGCGATGCTGCTGCGGAAATATCATGTTGAA	630								
QY	986	TGGCGGCTTTCTGATTCATCGACTGTGCGCGGCTGCTGCGGACCGCTATCAGGA	1045								
Db	631	TGGCGGCTTTCTGATTCATCGACTGTGCGCGGCTGCTGCGGACCGCTATCAGGA	690								
QY	1046	CATAGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTT	1105								
Db	691	CATAGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCGAATGGCTGACCGCTT	750								
QY	1106	CCTCGTGTTCACGATGCTGCGCTCCGATTCGACGCGATCGCTTCTATGCGCTTCT	1165								
Db	751	CCTCGTGTTCACGATGCTGCGCTCCGATTCGACGCGATCGCTTCTATGCGCTTCT	810								
QY	1166	TGACGAGTCTTCTGAG 1182									
Db	811	TGACGAGTCTTCTGAG 827									

RESULT 2
CK291519
LOCUS
DEFINITION
EST754233 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMC276 5'
end, mRNA sequence.
CK291519
CK291519.1 GI:39872047
VERSION

KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE 1 (Bases 1 to 804)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>
Seq primer: ANT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
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/clone="NBMC276"
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callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN		Query Match		9.9%; Score 794; DB 7; Length 804;		Best Local Similarity		100.0%; Pred. No. 3.7e-174;		Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	389	GATTGAACAAGATGATGACGACGATGCTGCTGTGATCGCGCGCTTGGGTGGAGAGCTATTGG	448								
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QY	449	CTATGACTGGGACAAACAGACAAATCGGCTGCTGTGATCGCGCGCTTGGGTGGAGAGCTATTGG	508								
Db	62	CTATGACTGGGACAAACAGACAAATCGGCTGCTGTGATCGCGCGCTTGGGTGGAGAGCTATTGG	121								
QY	509	GCAGGGGGCGCGGTTCTTTTGTCAAGACCGACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	568								
Db	122	GCAGGGGGCGCGGTTCTTTTGTCAAGACCGACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	181								
QY	569	GGAGGAGCAGCGCGGCTATCGTGGCTGGCCACGACGCGGCTTCTTCTGGAGCTGTGCT	628								
Db	182	GGAGGAGCAGCGCGGCTATCGTGGCTGGCCACGACGCGGCTTCTTCTGGAGCTGTGCT	241								
QY	629	CGAGCTTGTCACTGAAGCGGAAAGGACTGGGTGCTATTTGGCGAGAGTCCGCGGCGGCA	688								
Db	242	CGAGCTTGTCACTGAAGCGGAAAGGACTGGGTGCTATTTGGCGAGAGTCCGCGGCGGCA	301								
QY	689	TCTCTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	748								
Db	302	TCTCTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	361								
QY	749	GGGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	808								
Db	362	GGGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	421								

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Db |||||
QY 422 CGAGGAGCACACTACTCGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 481
Db |||||
QY 869 GCATCAGGGGCTCGGCGCAGCCGAACTGTCGCGAGGCTCAAGGGCGCATGCCGACGG 928
Db |||||
QY 482 GCATCAGGGGCTCGGCGCAGCCGAACTGTCGCGAGGCTCAAGGGCGCATGCCGACGG 541
Db |||||
QY 929 CGAGGATCTCGTCGTCACCCATCGGATGCTTCCGGAATATCATGTCGGAATATGG 988
Db |||||
QY 542 CGAGGATCTCGTCGTCACCCATCGGATGCTTCCGGAATATCATGTCGGAATATGG 601
Db |||||
QY 989 CCGCTTTTCTGATTCATGCACTGTGGCGGCTGTGGCGGACCGCTATCAGGACAT 1048
Db |||||
QY 602 CCGCTTTTCTGATTCATGCACTGTGGCGGCTGTGGCGGACCGCTATCAGGACAT 661
Db |||||
QY 1049 AGCGTTGTGCTACCCGTGATATGCTGAAGAGCTTGGCGGCGAATGGCTTCTTCT 1108
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QY 662 AGCGTTGTGCTACCCGTGATATGCTGAAGAGCTTGGCGGCGAATGGCTTCTTCT 721
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QY 1109 CGTCTTTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
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QY 722 CGTCTTTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 781
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QY 1169 CGAGTTCTTCTGAG 1182
Db |||||
QY 782 CGAGTTCTTCTGAG 795
Db |||||

RESULT 3

CK287297

LOCUS

DEFINITION EST750019 Nicotiana benthamiana mixed tissue cDNA library, EST 02-AUG-2004
normalized, full-length Nicotiana benthamiana cDNA clone NEMB815 5',
end, mRNA sequence.

ACCESSION

CK287297

KEYWORDS

EST.

ORGANISM

Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 856)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskiewicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST750020

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1. .856

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NEMB815"

/tissue_type="abiotic and biotic stress-treated leaves,

callus tissue and root tissue"

/lab_host="DH10B-Tona"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (*Pseudomonas syringae* pv tomato 12 hr;
Xanthomonas campestris pv *campestris* 12 hr, 18hr;
Pseudomonas syringae pv *phaseolicola* 18hr, and *Xanthomonas*
campestris pv *vesicatoria* 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.8e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 GATTCAACAAGATGCAATGCACGAGGTTCTCCGCGCGCTTGGTGGAGAGCTATTGG 448
Db |||||
QY 14 GATTGAAACAAGATGCAATGCACGAGGTTCTCCGCGCGCTTGGTGGAGAGCTATTGG 73
Db |||||
QY 449 CTATGACTGGGCACAAACAGACAATCGGCTGCTCTGATGCCGCGTGTTCGGCTCTCAGC 508
Db |||||
QY 74 CTATGACTGGGCACAAACAGACAATCGGCTGCTCTGATGCCGCGTGTTCGGCTCTCAGC 133
Db |||||
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QY 569 GCAGGAGCGAGCGGCTATCGTGGCTGGCCACAGCGGCGTTCCTTGGCAGCTGTGCT 628
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Db |||||
QY 629 CGAGTTTGTCTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGCGGAAGTGGCGGGCAGGA 313
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QY 689 TCTCTGTCTACTCACCTTCTCTCGCGAGAAAGTATCCATCATGGTGTGATGAATGCG 748
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QY 314 TCTCTGTCTACTCACCTTCTCTCGCGAGAAAGTATCCATCATGGTGTGATGAATGCG 373
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QY 749 GCGGCTGCATACGCTTGCATCGGCTACTGGCCANTTCGACCAACAAAGCAATCGCAT 808
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QY 374 GCGGCTGCATACGCTTGCATCGGCTACTGGCCANTTCGACCAACAAAGCAATCGCAT 433
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QY 434 CGAGCGAGCAGCTACTCGGATGGAAGCGGCTTGTGTCGATCAGGATGATCTGGACGAGA 493
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QY 869 GCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGAGGCTCAAGCGCGCATGCCGACGG 928
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QY 494 GCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGAGGCTCAAGCGCGCATGCCGACGG 553
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QY 929 CGAGGATCTCGTCGTCACCCATCGGATGCTTCCGGAATATCATGTCGGAATATGG 988
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QY 554 CGAGGATCTCGTCGTCACCCATCGGATGCTTCCGGAATATCATGTCGGAATATGG 613
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QY 989 CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGTGTGGCGGCGCTATCAGGACAT 1048
Db |||||
QY 614 CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGTGTGGCGGCGCTATCAGGACAT 673
Db |||||
QY 1049 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTTCCCT 1108
Db |||||
QY 674 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTTCCCT 733
Db |||||
QY 1109 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
Db |||||
QY 734 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 793
Db |||||
QY 1169 CGAGTTCTTCTGAG 1182
Db |||||
QY 794 CGAGTTCTTCTGAG 807
Db |||||

RESULT 4

CK287930

LOCUS

DEFINITION CK287930 910 bp mRNA linear EST 02-AUG-2004
EST750652 Nicotiana benthamiana mixed tissue cDNA library.

normalized, full-length Nicotiana benthamiana cDNA clone NEMBC75 5' end, mRNA sequence.

CK287930

CK287930.1 GI:39864940

EST

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 910)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST750653

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>.

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..910

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NEMBC75"

/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6 hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 910;

Best Local Similarity 100.0%; Pred. No. 3.8e-174;

Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

389 GATTGAACAGATGATGACGAGGTTCTCCGCGCGCTGGTGGAGAGGCTATTCCG 448

4 GATTGAACAGATGATGACGAGGTTCTCCGCGCGCTGGTGGAGAGGCTATTCCG 63

449 CTATGACTGGGCAACAGACAATCGGCTCTGTATGCCCGCGCTTCCTCCGAGC 508

64 CTATGACTGGGCAACAGACAATCGGCTCTGTATGCCCGCGCTTCCTCCGAGC 123

509 GCAGGGGGCGCGGTTCTTTTGTCAAGACCGACTGTCGGTGCCTGAATGAATGCA 568

124 GCAGGGGGCGCGGTTCTTTTGTCAAGACCGACTGTCGGTGCCTGAATGAATGCA 183

569 GCAGGAGGAGCGCGGCTATGTTGGCTGCCACGAGCGGCTTCCTCCGAGCTGTCT 628

184 GCAGGAGGAGCGCGGCTATGTTGGCTGCCACGAGCGGCTTCCTCCGAGCTGTCT 243

629 CGACGTTGTCAGTGAAGCGGAGGAGTGGCTGCTATTGGCGAAGTCCCGGGCAGGA 688

244 CGACGTTGTCAGTGAAGCGGAGGAGTGGCTGCTATTGGCGAAGTCCCGGGCAGGA 303

689 TCTCTGTGTCATCTCAGCTTGTCTCTGCCGAGAAAGTATCCATCATGCTGATGCAATGCC 748

Db 304 TCTCTGTGTCATCTCAGCTTGTCTCCGCGAGAAAGTATCCATCATGCTGATGCAATGCC 363

Qy 749 GCGGCTGCATACGCTTGTATCCGGTCTACCTGCCATTCGACCAAGCGAAACATCGCAT 808

Db 364 GCGGCTGCATACGCTTGTATCCGGTCTACCTGCCATTCGACCAAGCGAAACATCGCAT 423

Qy 809 CGAGCGACGCTATCTCGATGGAAGCCGGTCTTCTCGATCAGGATGATCTGACGAGA 868

Db 424 CGAGCGACGCTATCTCGATGGAAGCCGGTCTTCTCGATCAGGATGATCTGACGAGA 483

Qy 869 GCATCAGGGGCTCGCGCCAGCGAACTGTTCCGAGGCTCAAGCGCGCGCATGCCGACGG 928

Db 484 GCATCAGGGGCTCGCGCCAGCGAACTGTTCCGAGGCTCAAGCGCGCGCATGCCGACGG 543

Qy 929 CGAGGATCTCGTCTGTCGACCCATGCGGATGCTGCTTGGCGAATATCATGGTGAATAATGG 988

Db 544 CGAGGATCTCGTCTGTCGACCCATGCGGATGCTGCTTGGCGAATATCATGGTGAATAATGG 603

Qy 989 CCGCTTTTCTGGATTCATCGACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACAT 1048

Db 604 CCGCTTTTCTGGATTCATCGACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACAT 663

Qy 1049 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGCGTTCCT 1108

Db 664 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGCGTTCCT 723

Qy 1109 CGTGTCTTTACGGTATCGCGCTCCCGATTCGAGCGCATCGCTTATCGCCTTCTTGA 1168

Db 724 CGTGTCTTTACGGTATCGCGCTCCCGATTCGAGCGCATCGCTTATCGCCTTCTTGA 783

Qy 1169 CGAGTTCTTCTGAG 1182

Db 784 CGAGTTCTTCTGAG 797

RESULT 5

CK291799 933 bp mRNA linear EST 02-AUG-2004

CK291799

LOCUS

EST754513 Nicotiana benthamiana mixed tissue cDNA library,

normalized, full-length Nicotiana benthamiana cDNA clone NEMC477 5'

end, mRNA sequence.

CK291799

CK291799.1 GI:39872608

EST

KEYWORDS

SOURCE

Nicotiana benthamiana

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 933)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST754514

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>.

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

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/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NEMC477"

/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"

FEATURES

source

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 933;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAAGATGATTGCACGACGAGTTCCTCCGCCGCTTGGTGGAGAGGCTATTTCGG 448
DB |||||
QY 449 CTATGACTGGGCACACAGACAATCGGCTGCTCTCATGCCGCCGCTTCCGCTCTCAGC 508
DB |||||
QY 106 CTATGACTGGGCACACAGACAATCGGCTGCTCTCATGCCGCCGCTTCCGCTCTCAGC 165
DB |||||
QY 509 GCAGGGGCCCGGTTCTTTTGTCAAGACGACCTGTCCGCTGCCCTGAATGAATGCA 568
DB |||||
QY 166 GCAGGGGCCCGGTTCTTTTGTCAAGACGACCTGTCCGCTGCCCTGAATGAATGCA 225
QY 569 GCAGGACGACGGGCTATCGTGGCTGGCCACGACGGCGTTCCTTGGGAGCTGTGCT 628
DB |||||
QY 226 GGAAGGACGACGGGCTATCGTGGCTGGCCACGACGGCGTTCCTTGGGAGCTGTGCT 285
DB |||||
QY 629 CGAGCTTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGGAAGTCCATCATGCTGATGCAATGCG 748
DB |||||
QY 346 TCTCTGTCTATCTACCTTGTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAATGCG 405
QY 749 GCGGCTGATACGCTTGCATCGGCTACCTGCGCAATGGCAACCAAGCAAACTATCGAT 808
DB |||||
QY 406 GCGGCTGATACGCTTGCATCGGCTACCTGCGCAATGGCAACCAAGCAAACTATCGAT 465
QY 809 CGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGAGA 868
DB |||||
QY 466 CGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGAGA 525
QY 869 GCATCAGGGCTGCGCCAGCGCACTGTTGCGCAGGCTCAAGCGCGCATGCCCGACGG 928
DB |||||
QY 526 GCATCAGGGCTGCGCCAGCGCACTGTTGCGCAGGCTCAAGCGCGCATGCCCGACGG 585
QY 929 CGAGGATCTCGTGTGACCCATCGCATGCTGCTTGGCGCAATATCATGTTGGAATGG 988
DB |||||
QY 586 CGAGGATCTCGTGTGACCCATCGCATGCTGCTTGGCGCAATATCATGTTGGAATGG 645
QY 989 CCGCTTTTCTGGATTCATCGACTGTGGCGGCTGGGTTGGCGGACCGCTATCAGGACAT 1048
DB |||||
QY 646 CCGCTTTTCTGGATTCATCGACTGTGGCGGCTGGGTTGGCGGACCGCTATCAGGACAT 705
QY 1049 AGCGTTGGCTACCGGTGATATTCGTAAGAGCTTGGCGGCAATGGGCTGACCGCTTCCT 1108
DB |||||
QY 706 AGCGTTGGCTACCGGTGATATTCGTAAGAGCTTGGCGGCAATGGGCTGACCGCTTCCT 765
QY 1109 CGTGTCTTACGGTATCGCGCTCCGATTCGACGCGCATCGCTTCTATCGCTTCTTGA 1168
DB |||||
QY 766 CGTGTCTTACGGTATCGCGCTCCGATTCGACGCGCATCGCTTCTATCGCTTCTTGA 825
QY 1169 CGAGTTCTTCTGAG 1182
DB |||||
QY 826 CGAGTTCTTCTGAG 839

RESULT 6

CK256977

LOCUS

DEFINITION

CK256977

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CK256977 936 bp mRNA linear EST 30-JUL-2004
EST740614 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POC170 5' end, mRNA sequence.

CK256977 1 GI:39813957

EST.

Solanum tuberosum (potato)

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 936)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from potato callus tissue

Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..936

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POCD170"

/tissue_type="callus"

/lab_host="DH10B-Tona"

/clone_lib="potato callus cDNA library, normalized and

full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Solanum tuberosum var.

Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 936;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 GATTGAACAAGATGATTGCACGACGAGTTCCTCCGCCGCTTGGTGGAGAGGCTATTTCGG 448
DB |||||
QY 449 CTATGACTGGGCACACAGACAATCGGCTGCTCTCATGCCGCCGCTTCCGCTCTCAGC 508
DB |||||
QY 509 GCAGGGGCCCGGTTCTTTTGTCAAGACGACCTGTCCGCTGCCCTGAATGAATGCA 568
DB |||||
QY 134 GCAGGGGCCCGGTTCTTTTGTCAAGACGACCTGTCCGCTGCCCTGAATGAATGCA 193
QY 569 GGAAGGACGACGGCTATCGTGGCTGGCCACGACGCGGCTTCCTTGGCGAGCTGTGCT 628
DB |||||
QY 194 GGAAGGACGACGGCTATCGTGGCTGGCCACGACGCGGCTTCCTTGGCGAGCTGTGCT 253
QY 629 CGAGCTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGGCGAAGTGCCGGGCGAGGA 688
DB |||||
QY 254 CGAGCTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGGCGAAGTGCCGGGCGAGGA 313
QY 689 TCTCTGTCTATCTACCTTGTCTCCCTCCGAGAAAGTATCCATCATGCTGCTGATGCAATGCG 748
DB |||||
QY 314 TCTCTGTCTATCTACCTTGTCTCCCTCCGAGAAAGTATCCATCATGCTGCTGATGCAATGCG 373
QY 749 GCGGCTGTACATCGCTTGTATCCCGCTACCTGCCCATTTCCGACCAAGCGCAATCGCAT 808
DB |||||
QY 374 GCGGCTGTACATCGCTTGTATCCCGCTACCTGCCCATTTCCGACCAAGCGCAATCGCAT 433

QY	809	CGAGGACAGTACTCGATGGAAGCCGGTCTTCTCGATCAGGATGATCTGACGAAGA	868
Db	434	CGAGGACAGTACTCGATGGAAGCCGGTCTTCTCGATCAGGATGATCTGACGAAGA	493
QY	869	GCATCAGGGGCTCGGCGCAGCCGAACCTGTTCCCGAGGCTCAAGGCGCGCATCCCGACGG	928
Db	494	GCATCAGGGGCTCGGCGCAGCCGAACCTGTTCCCGAGGCTCAAGGCGCGCATCCCGACGG	553
QY	929	CGAGGATCTGTCGTCGACCCATGGCGATCGCTTTCGCAATATCATGTCGGAATGG	988
Db	554	CGAGGATCTGTCGTCGACCCATGGCGATCGCTTTCGCAATATCATGTCGGAATGG	613
QY	989	CCGCTTTCTCGATTCATCGACTGTCGCGGCTGGGTGGCGGACCGCTATCAGGACAT	1048
Db	614	CCGCTTTCTCGATTCATCGACTGTCGCGGCTGGGTGGCGGACCGCTATCAGGACAT	673
QY	1049	AGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCAATGGGCTACCGCTTCT	1108
Db	674	AGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCAATGGGCTACCGCTTCT	733
QY	1109	CGTGTCTTACGATCGCGCTCCGATTCGAGAGCTTGGCGGCAATGGGCTTCTTGA	1168
Db	734	CGTGTCTTACGATCGCGCTCCGATTCGAGAGCTTGGCGGCAATGGGCTTCTTGA	793
QY	1169	CGAGTTCTTCTGAG	1182
Db	794	CGAGTTCTTCTGAG	807
RESULT 7			
CK298208		947 bp mRNA linear EST 02-AUG-2004	
LOCUS		EST760922 Nicotiana benthamiana mixed tissue cDNA library,	
DEFINITION		normalized, full-length Nicotiana benthamiana cDNA clone NEMDE30 5'	
ACCESSION		end, mRNA sequence.	
VERSION		CK298208.1 GI:39885354	
SOURCE		EST.	
KEYWORDS		Nicotiana benthamiana	
ORGANISM		Nicotiana benthamiana	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
TITLE		asterids; lamiales; Solanales; Solanaceae; Nicotiana.	
JOURNAL		1 (bases 1 to 947)	
COMMENT		Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,	
FEATURES		Skaskiewicz, B., Jin, H. and Baker, S.	
source		Generation of EST sequences from Nicotiana benthamiana	
		Other ESTs: EST760923	
		Contact: Robin Buell	
		The Institute for Genomic Research	
		9712 Medical Center Dr, Rockville, MD 20850, USA	
		Email: potato-array@tigr.org	
		Clones can be requested from the University of Arizona Genomics	
		Institute via http://genome.arizona.edu/orders/	
		Seq primer: ANT TAG GTG ACA CTA TAG.	
		location/Qualifiers	
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		/db_xref="taxon:4100"	
		/clone="NEMDE30"	
		/tissue_type="abiotic and biotic stress-treated leaves,	
		callus tissue and root tissue"	
		/lab_host="PH10B-TonA"	
		/clone_lib="Nicotiana benthamiana mixed tissue cDNA	
		library, normalized, full-length"	
		/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;	
		supplier: RNA was isolated from Nicotiana benthamiana	
		tissues that include callus, roots from liquid culture	
		grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),	
		cold-stressed leaves (5 C 3 hr, 6hr), and pathogen	
		challenged leaves (Pseudomonas syringae pv tomato 12 hr;	

RESULT 8
CK283361
LOCUS

DEFINITION
EST746083 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5'

CK283361
954 bp mRNA linear EST 02-AUG-2004

Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match	9.9%;	Score 794;	DB 7;	Length 947;
Best Local Similarity	100.0%;	Pred. No. 3.9e-174;	Mismatches 0;	Gaps 0;
Matches 794;	Conservative 0;			
QY	389	GATTGAACAAGATGATTGACGACAGGTCTCCGCGCGCTTGGGTGGAGAGGCTATTCGG	448	
Db	17	GATTGAACAAGATGATTGACGACAGGTCTCCGCGCGCTTGGGTGGAGAGGCTATTCGG	76	
QY	449	CTATGACTGGGCACAAACAGACAATCGGCTGCTCTGATGCGCGCTTCCGGCTGTGCT	508	
Db	77	CTATGACTGGGCACAAACAGACAATCGGCTGCTCTGATGCGCGCTTCCGGCTGTGCT	136	
QY	509	GAAGGGGCGCGCGCTTCTTTTGTCAAGACCGACCTGTCGCGTCCCTTGAATGAATGCA	568	
Db	137	GAAGGGGCGCGCGCTTCTTTTGTCAAGACCGACCTGTCGCGTCCCTTGAATGAATGCA	196	
QY	569	GGACGAGGCGCGCGCTATCGTGGCTGGCCACGACGGGCTTCCCTTGGCAGCTGTGCT	628	
Db	197	GGACGAGGCGCGCGCTATCGTGGCTGGCCACGACGGGCTTCCCTTGGCAGCTGTGCT	256	
QY	629	CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGGGGGAAGTCCGGGGCAGGA	688	
Db	257	CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGGGGGAAGTCCGGGGCAGGA	316	
QY	689	TCTCCTGTCTATCTACTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG	748	
Db	317	TCTCCTGTCTATCTACTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG	376	
QY	749	CGCGCTGCATACGCTTGCATCGGCTACCTGCCATTCGACCAACGAGCAACATCGCAT	808	
Db	377	CGCGCTGCATACGCTTGCATCGGCTACCTGCCATTCGACCAACGAGCAACATCGCAT	436	
QY	809	CGACGAGCAGCTACTCGGATGGAAGCCGGTCTTGTCTGATCAGGATGATCTGACGAAGA	868	
Db	437	CGACGAGCAGCTACTCGGATGGAAGCCGGTCTTGTCTGATCAGGATGATCTGACGAAGA	496	
QY	869	GCATCAGGGGCTCGCGCAGCCGACCTGTCGCCAGGCTCAAGGCGCGCATGCCCGCAGG	928	
Db	497	GCATCAGGGGCTCGCGCAGCCGACCTGTCGCCAGGCTCAAGGCGCGCATGCCCGCAGG	556	
QY	929	CGAGGATCTCGTCTGACCCATGCGGATCGCTGCTTCCGGAATATCATGTTGGAATAATGG	988	
Db	557	CGAGGATCTCGTCTGACCCATGCGGATCGCTGCTTCCGGAATATCATGTTGGAATAATGG	616	
QY	989	CCGCTTTTCTGATTTCATCGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAGGACAT	1048	
Db	617	CCGCTTTTCTGATTTCATCGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAGGACAT	676	
QY	1049	AGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCT	1108	
Db	677	AGCGTTGGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCT	736	
QY	1109	CGTGTCTTACGATTCGCGCGCTCCGATTCGAGCGGCTATTCGCTTCTATCGCTTCTTGA	1168	
Db	737	CGTGTCTTACGATTCGCGCGCTCCGATTCGAGCGGCTATTCGCTTCTATCGCTTCTTGA	796	
QY	1169	CGAGTTCTTCTGAG	1182	
Db	797	CGAGTTCTTCTGAG	810	

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end, mRNA sequence.
ACCESSION CK2833361
VERSION CK2833361.1 GI:39855898
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 954)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST746084
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
7912 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
source
1..954
Location/Qualifiers
    /organism="Nicotiana benthamiana"
    /mol_type="mRNA"
    /db_xref="taxon:4100"
    /clones="NBMA650"
    /tissue_type="abiotic and biotic stress-treated leaves,
    callus tissue and root tissue"
    /lab_host="DH10B-Tona"
    /clone_lib="Nicotiana benthamiana mixed tissue cDNA
    library, normalized, full-length"
    /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
    supplier: RNA was isolated from Nicotiana benthamiana
    grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
    cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
    challenged leaves (Pseudomonas syringae pv tomato 12 hr;
    Xanthomonas campestris pv campestris 12 hr, 18hr;
    Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
    campestris pv vesicatoria 18hr). RNA was isolated from
    these tissues and pooled in approximately equal molar
    amounts."
ORIGIN
Query Match 9.9%; Score 794; DB 7; Length 954;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 GATTGAACAAAGATGGATTGACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTTCGG 448
DB 14 GATTGAACAAAGATGGATTGACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTTCGG 73
QY 449 CTATGACTGGGACACAGACATCGGCTGCTGTGATGCCCGCTGTTCCGGCTGTGAGC 508
DB 74 CTATGACTGGGACACAGACATCGGCTGCTGTGATGCCCGCTGTTCCGGCTGTGAGC 133
QY 509 GCAGGGGGCCCGCGGTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAATGAATGCA 568
DB 134 GCAGGGGGCCCGCGGTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAATGAATGCA 193
QY 569 GGACGAGGCGCGCGCTATCGTGGCTGGCCACGAGCGGCTTCCTTGGCGAGCTGTGCT 628
DB 194 GGACGAGGCGCGCGCTATCGTGGCTGGCCACGAGCGGCTTCCTTGGCGAGCTGTGCT 253
QY 629 CGACGTTGCTCACTGAAGCGGGAAGGACTGGTGTCTATTGGCGAAGTCCCGGGCAGGA 688
DB 254 CGACGTTGCTCACTGAAGCGGGAAGGACTGGTGTCTATTGGCGAAGTCCCGGGCAGGA 313
QY 689 TCTCTGTGTCATCTCACTTGTCTTCCCGGAGAAAGTATCCATCATGCTGATGCAATGG 748
DB 314 TCTCTGTGTCATCTCACTTGTCTTCCCGGAGAAAGTATCCATCATGCTGATGCAATGG 373

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QY 749 GCGGCTGCATACGCTTGATTCGGCTACCTGCCCATTCGACCAAGCGAAACATCGCAT 808
DB 374 GCGGCTGCATACGCTTGATTCGGCTACCTGCCCATTCGACCAAGCGAAACATCGCAT 433
QY 809 CGAGCGACACGCTACTCGGATGGAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGA 868
DB 434 CGAGCGACACGCTACTCGGATGGAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGA 493
QY 869 GCATCAGGGGCTCGCGCCAGCCGCAACTGTTCCGACAGGCTCAAGGCGCCATGCCGACGG 928
DB 494 GCATCAGGGGCTCGCGCCAGCCGCAACTGTTCCGACAGGCTCAAGGCGCCATGCCGACGG 553
QY 929 CGAGGATCTCGTGTGACCCATGCGCATGCTGCTTCCGCAATATCATGGTGGAAATGG 988
DB 554 CGAGGATCTCGTGTGACCCATGCGCATGCTGCTTCCGCAATATCATGGTGGAAATGG 613
QY 989 CCGCTTTTCTCGATTTCATCGACTGTCGGCGCTGGGTGTGGCGACCGCTATCGGACAT 1048
DB 614 CCGCTTTTCTCGATTTCATCGACTGTCGGCGCTGGGTGTGGCGACCGCTATCGGACAT 673
QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCC 1108
DB 674 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCC 733
QY 1109 GGTGCTTACGATTCGCGCTCCGATTCGACGCGCATCCCTTCTATCGCCTTCTTGA 1168
DB 734 GGTGCTTACGATTCGCGCTCCGATTCGACGCGCATCCCTTCTATCGCCTTCTTGA 793
QY 1169 CGAGTTCTTCTGAG 1182
DB 794 CGAGTTCTTCTGAG 807

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RESULT 9
LOCUS CK288185
DEFINITION CK288185
            811 bp mRNA linear EST 02-AUG-2004
            EST750907 Nicotiana benthamiana mixed tissue cDNA library,
            normalized, full-length Nicotiana benthamiana cDNA clone NBMB61 5'
            end, mRNA sequence.
ACCESSION CK288185
VERSION CK288185.1 GI:39865462
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 811)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
source
1..811
Location/Qualifiers
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    /db_xref="taxon:4100"
    /clones="NBMB61"
    /tissue_type="abiotic and biotic stress-treated leaves,
    callus tissue and root tissue"
    /lab_host="DH10B-Tona"
    /clone_lib="Nicotiana benthamiana mixed tissue cDNA
    library, normalized, full-length"
    /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
    supplier: RNA was isolated from Nicotiana benthamiana

```

tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Xanthomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 9.7%; Score 778.8; DB 7; Length 811;
Best Local Similarity 99.7%; Pred. No. 1.3e-170;
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CATGATTGAACAGATGGATTCCACGCGGTTCTCGCGCGCTTGGTGGAGAGGCTATT 445
DB 30 CATGATTGAACAGATGGATTCCACGCGGTTCTCGCGCGCTTGGTGGAGAGGCTATT 89

QY 446 CGGCTATGATGGGACACACAGACATCGGCTGCTGATGCGCGCTTCCGGCTGTC 505
DB 90 CGGCTATGATGGGACACACAGACATCGGCTGCTGATGCGCGCTTCCGGCTGTC 149

QY 506 AGCGAGGGCGCGCGGCTTTTCTTCTCAAGACCGACCTGTCCGGTCCCTGATGAAT 565
DB 150 AGCGAGGGCGCGCGGCTTTTCTTCTCAAGACCGACCTGTCCGGTCCCTGATGAAT 209

QY 566 GCAGGACGAGGCGCGGCTATGCTGGTGGCCACGAGGGGTTCTTGGCAGCTGT 625
DB 210 GCAGGACGAGGCGCGGCTATGCTGGTGGCCACGAGGGGTTCTTGGCAGCTGT 269

QY 626 GCTCGAGCTGTCTCACTGAAGCGGAGGAGGACTGGCTGCTATTGGCGGAAGTCCGGGCA 685
DB 270 GCTCGAGCTGTCTCACTGAAGCGGAGGAGGACTGGCTGCTATTGGCGGAAGTCCGGGCA 329

QY 686 GGATCTCTCTCATCTCACCTTGTCTCGCGGAGAAAGTATCCATCATGCTCATGCAAT 745
DB 330 GGATCTCTCTCATCTCACCTTGTCTCGCGGAGAAAGTATCCATCATGCTCATGCAAT 389

QY 746 CGCGCGGCTGCATACGCTTATCGGCTGATCGGCTACTGCGCCATTCGACCAACGGAACATCG 805
DB 390 CGCGCGGCTGCATACGCTTATCGGCTACTGCGCCATTCGACCAACGGAACATCG 449

QY 806 CATCGAGCAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGA 865
DB 450 CATCGAGCAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGA 509

QY 866 AGAGCATCAGGGGCTCGCGCGCAGCGCAACTGTTCGCCAGGCTCAAGCGCGCATGCCGA 925
DB 510 AGAGCATCAGGGGCTCGCGCGCAGCGCAACTGTTCGCCAGGCTCAAGCGCGCATGCCGA 569

QY 926 CGGCGAGGATCTGCTGATGACCCATGGGATGCTGCTTGGCGGAATATCATGTTGGA 985
DB 570 CGGCGATGATCTGCTGATGACCCATGGGATGCTGCTTGGCGGAATATCATGTTGGA 629

QY 986 TGGCGGCTTTCTGGATTCATCGACTGCGCGGCTGGGCTGGCGGACCGCTATCAGGA 1045
DB 630 TGGCGGCTTTCTGGATTCATCGACTGCGCGGCTGGGCTGGCGGACCGCTATCAGGA 689

QY 1046 CATAGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGGAATGGGCTGACCGCTT 1105
DB 690 CATAGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGGAATGGGCTGACCGCTT 749

QY 1106 CTTGCTGTTTACGCTATCGGCTGCCGATTCGAGCGCATCGCTTCTATCGCCTTCT 1165
DB 750 CTTGCTGTTTACGCTATCGGCTGCCGATTCGAGCGCATCGCTTCTATCGCCTTCT 809

QY 1166 TG 1167
DB 810 TG 811

RESULT 10

CK288711
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

CK288711 878 bp mRNA linear EST 02-AUG-2004
EST751433 Nicotiana benthamiana mixed tissue cDNA library, NEMBI49 5' normalized, full-length Nicotiana benthamiana cDNA clone NEMBI49 5' end, mRNA sequence.
CK288711 GI:39866496
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 878)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H., and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..878
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
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/clone="NEMBI49"
/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 7.3%; Score 587; DB 7; Length 878;
Best Local Similarity 100.0%; Pred. No. 9.3e-126;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 596 GGCCACACGCGGCTTCTTCCGCGAGTGTCTCGAGTGTCTCACTGCTCAAGCGGAGGGA 655
DB 1 GGCCACACGCGGCTTCTTCCGCGAGTGTCTCGAGTGTCTCACTGCTCAAGCGGAGGGA 60

QY 656 CTGGCTGCTATTGGGCGAAGTGC CGGGCGAGGATCTCTGTCATCTCACTTGTCTCTGC 715
DB 61 CTGGCTGCTATTGGGCGAAGTGC CGGGCGAGGATCTCTGTCATCTCACTTGTCTCTGC 120

QY 716 CGAGAAAGTATCCATCATGGCTGATGCATGCGGCGCTGCATAGCTTGTATCCGGCTAC 775
DB 121 CGAGAAAGTATCCATCATGGCTGATGCATGCGGCGCTGCATAGCTTGTATCCGGCTAC 180

QY 776 CTGGCCATTTCACCAACGCAACATCGCATCGAGCGACGATCTCGATCGGATGGAAGC 835
DB 181 CTGGCCATTTCACCAACGCAACATCGCATCGAGCGACGATCTCGATCGGATGGAAGC 240

QY 836 CGGTCTTGTGATCAGGATGATCTGGACGAAGAGATCAGGGGCTCGCGCGCGGAACT 895
DB 241 CGGTCTTGTGATCAGGATGATCTGGACGAAGAGATCAGGGGCTCGCGCGCGGAACT 300


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QY 896 GTTCGCCAGGCTCAAGCGCGGATCGCCGACGCGGAGGATCTCGTGTGACCCCATGGCGA 955
Db 301 GTTCGCCAGGCTCAAGCGCGGATCGCCGACGCGGAGGATCTCGTGTGACCCCATGGCGA 360
QY 956 TGCCTGCTTTCGCGAATATCATGCTGGAATAATGCGCGCTTTCTTGGATTTCATCGACTGTGG 1015
Db 361 TGCCTGCTTTCGCGAATATCATGCTGGAATAATGCGCGCTTTCTTGGATTTCATCGACTGTGG 420
QY 1016 CCGGCTGGGTGGCGGACCGTATCAGGACATAGCGTTGGTACCCGCTGATATTCCTGA 1075
Db 421 CCGGCTGGGTGGCGGACCGTATCAGGACATAGCGTTGGTACCCGCTGATATTCCTGA 480
QY 1076 AGAGCTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTAGGTTAGGTTAGCGCGCTCCCGA 1135
Db 481 AGAGCTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTTACGGTTATCGCGCTCCCGA 540
QY 1136 TTGCGAGCGCATCGCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAG 1182
Db 541 TTGCGAGCGCATCGCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAG 587

RESULT 11
AQ361914 789 bp DNA linear GSS 03-FEB-1999
LOCUS clone mgxb0005K01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
DEFINITION clone mgxb0005K01f, genomic survey sequence.
ACCESSION AQ361914
VERSION AQ361914.1 GI:4211753
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 789)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCATATAGGG
Class: BAC ends
High quality sequence start: 41
High quality sequence stop: 392.
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Location/Qualifiers
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1..789
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
Notes: Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
ORIGIN

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Query Match 7.2%; Score 577.4; DB 8; Length 789;
Best Local Similarity 97.8%; Pred. No. 1.6e-123;
Matches 584; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 581 GCGGCTATCGTGGCTGGCCACGACGGGCGTTCTCTCGCGAGCTGTGCTCGACGTTCTCAC 640
Db 39 GCGGCTATCGTGGCTGGCCACGACGGGCGTTCTCTCGCGAGCTGTGCTCGACGTTCTCAC 98
QY 641 TGAAGCGGGAAGGAGTGTGCTCTATTGGGCGAAGTTCGCGGGGCGAGATCTCTGTCTATC 700
Db 99 TGAAGCGGGAAGGAGTGTGCTCTATTGGGCGAAGTTCGCGGGGCGAGATCTCTGTCTATC 158
QY 701 TCACCTTGTCTCTCGCGAGAAAGTATCCATCATGCTGTATGCAATCGCGCGGTGTGATAC 760
Db 159 TCACCTTGTCTCTCGCGAGAAAGTATCCATCATGCTGTATGCAATCGCGCGGTGTGATAC 218
QY 761 GUTTGATCCGGCTACCTTGCCTCCATTCGACCAACGCGAAACATCGCATCGAGGAGCAG 820
Db 219 GUTTGATCCGGCTACCTTGCCTCCATTCGACCAACGCGAAACATCGCATCGAGGAGCAG 278
QY 821 TACTCGGATGGAAGCGGCTTGTGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCT 880
Db 279 TACTCGGATGGAAGCGGCTTGTGTCGATCAGGATGATCTGGAAGAGCATCAGGGGCT 338
QY 881 CGCGCCAGCCGAACGTTCGCGCAGGCTCAAGCGCGCATGCCCGACGCGGAGATCTCGT 940
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QY 941 CGTGACCATGCGGATGCTTGTCCGAATATCATGCTGGAAATGCGCGCTTCTGCG 1000
Db 399 CGTGACCATGCGGATGCTTGTCCGAATATCATGCTGGAAATGCGCGCTTCTGCG 458
QY 1001 ATTTCATGACTGTGCGCGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC 1060
Db 459 ATTTCATGACTGTGCGCGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC 518
QY 1061 CCGTGATATTGCTCAAGAGCTTGGCGGGAATGGGCTACCGCTTCTGTGCTTTACGG 1120
Db 519 CCGTGATATTGCTCAAGAGCTTGGCGGGAATGGGCTACCGCTTCTGTGCTTTACGG 578
QY 1121 TATCGCGCTCCCGATTGCGAGCGCATGCTTCTATCGGCTTCTTACGAGTTCTT 1177
Db 579 TATCGCGCTCCCGATTGCGAGCGCATGCTTCTATCGGCTTCTTACGAGGNTTTT 635

RESULT 12
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LOCUS clone mgxb0009J05f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
DEFINITION clone mgxb0009J05f, genomic survey sequence.
ACCESSION AQ398387
VERSION AQ398387.1 GI:4369414
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 620)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCATATAGGG
Class: BAC ends
High quality sequence stop: 187.

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/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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source
1. .549
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/clone="NF32c08f44"
/tissue_type="shoot"
/lab_host="E. coli"
/clone_lib="Tall Fescue PI283316 44 deg C Heat Stress SSH
cDNA"
/note="Vector: PCR 2.1-TOPO; Site 1: EcoR I; Site 2: EcoR
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CK801630
CK801630.1 GI:43400943
EST.
Schedonorus arundinaceus (Festuca arundinacea)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poaceae; Schedonorus.
1. (bases 1 to 549)
Zhang, Y., Zwonitzer, J.C., Chekhovskiy, K., May, G.D. and Mian, M.A.R.
A functional genomics approach for identification of heat tolerance
genes in tall fescue
(in) Hopkins, A., Wang, Z.Y., Mian, R., Sledge, M. and Barker, R.R.
(eds.), MOLECULAR BREEDING OF FORAGE AND TURF, Kluwer Acad. Pub. 0,
87-96 (2003)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact: Dr. Rouf Mian (rmian@nobel.org) regarding clone availability
Seq primer: M13 reverse primer
High quality sequence stop: 470.

Query Match 7.0%; Score 559.8; DB 8; Length 620;
Best Local Similarity 98.8%; Pred. No. 2e-119; Indels 0; Gaps 0;
Matches 564; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 609 GTTCTTGGCAGCTGTGCTCGACGTTGTCTCACTGAAGCGGGAAGGAGCTGGCTGCTATTG 668
DB 1 GTTCTTGGCAGCTGTGCTCGACGTTGTCTCACTGAAGCGGGAAGGAGCTGGCTGCTATTG 60
QY 669 GCGCAAGTCCGCGGCGAGGATCTCTGTGATCTCACTTCTCTCTGCGGAGAAAGTATCC 728
DB 61 GCGCAAGTCCGCGGCGAGGATCTCTGTGATCTCACTTCTCTCTGCGGAGAAAGTATCC 120
QY 729 ATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGTATCGGCTACTGCCCATTCGAC 788
DB 121 ATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGTATCGGCTACTGCCCATTCGAC 180
QY 789 CACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATG 848
DB 181 CACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATG 240
QY 849 CAGGATGATCTGGAACGAGCATCAGGGGCTCGCGGCGAGCACTTTCGCCAGGCTC 908
DB 241 CAGGATGATCTGGAACGAGCATCAGGGGCTCGCGGCGAGCACTTTCGCCAGGCTC 300
QY 909 AAGCGGCGCATGCGCGGCGAGGATCTCTGTGATCTCACTGATGCGGATGCGGCTG 968
DB 301 AAGCGGCGCATGCGCGGCGAGGATCTCTGTGATCTCACTGATGCGGATGCGGCTG 360
QY 969 AATATCATGTTGGAATAATGGCGCTTTTCTGATTCATCGATGTCGCGGCTGGTGTG 1028
DB 361 AATATCATGTTGGAATAATGGCGCTTTTCTGATTCATCGATGTCGCGGCTGGTGTG 420
QY 1029 CGGACCGCTATCAGGACATGCGGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1088
DB 421 CGGACCGCTATCAGGACATGCGGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 480
QY 1089 GAATGGGCTGACCGGCTTCTCTGCTTACGGTATCGCGGCTGCCGATTCGAGCGCATC 1148
DB 481 GAATGGGCTGACCGGCTTCTCTGCTTACGGTATCGCGGCTGCCGATTCGAGCGCATC 540
QY 1149 GCCTTCTATCGGCTTCTTTCAGCAGTCTTCT 1179
DB 541 GCCTTCTATCGGCTTCTTTCAGCAGTCTTCTT 571

RESULT 13
CK801630
LOCUS
DEFINITION
CK801630 549 bp mRNA linear EST 26-FEB-2004
NF32c08f44.r1 Tall Fescue PI283316 44 deg C Heat Stress SSH cDNA
Schedonorus arundinaceus cDNA clone NF32c08f44 5', mRNA sequence.

Query Match 6.8%; Score 542.4; DB 7; Length 549;
Best Local Similarity 99.8%; Pred. No. 2.2e-115;
Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 556 TGAATGAATCGCAGGACGAGCGCGGTATCGTGGCTGGCCACGACGCGGCTTCCTT 615
DB 6 TGAATGAATCGCAGGACGAGCGCGGTATCGTGGCTGGCCACGACGCGGCTTCCTT 65
QY 616 GCGCAGCTGTCTGAGCTGTGTCTCACTGAAGCGGGAAGGAGTGTCTGTTGGCGGAAG 675
DB 66 GCGCAGCTGTCTGAGCTGTGTCTCACTGAAGCGGGAAGGAGTGTCTGTTGGCGGAAG 125
QY 676 TGCCGGGCGAGGATCTCTGTCTCATCTCACTTGTCTTCCGAGAAAGTATCCATCATGG 735
DB 126 TGCCGGGCGAGGATCTCTGTCTCATCTCCACCTTGTCTTCCGAGAAAGTATCCATCATGG 185
QY 736 CTGATGCAATCGCGGCTGCATACGCTTGTATCGGCTTACCTGCCATTCGACCAACCAAG 795
DB 186 CTGATGCAATCGCGGCTGCATACGCTTGTATCGGCTTACCTGCCATTCGACCAACCAAG 245
QY 796 CGAAACATCGCATCAGCGGACGCTACTCGGATGGAAGCGGCTTGTTCGATCAGGATG 855
DB 246 CGAAACATCGCATCAGCGGACGCTACTCGGATGGAAGCGGCTTGTTCGATCAGGATG 305
QY 856 ATCTCGACGAGAGCATCAGGGGCTCGGCGCACGCGAACTGTTCGCGAGGCTCAAGCGGC 915
DB 306 ATCTCGACGAGAGCATCAGGGGCTCGGCGCACGCGAACTGTTCGCGAGGCTCAAGCGGC 365
QY 916 GCATGCCGACCGCGAGGATCTCTGCTGTCGACCCATGGCGATCGCTTCCGATATCA 975
DB 366 GCATGCCGACCGCGAGGATCTCTGCTGTCGACCCATGGCGATCGCTTCCGATATCA 425
QY 976 TGGTGAAATGCGCGCTTTTCTGATTCATCGACTGTGCGCGGCTGGGTGTGGCGGACC 1035

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Db      426  TGGTGAATAATGCCCGCTTTTCGGATTTCATCGACTGTGCCGGCTGGGTGTGGCGACC 485
QY      1036  GCTATCAGGACATAGCGTTGGCTACCGTGATATTCCTGAAGAGCTTTGGCGCGATGGG 1095
Db      486  GCTATCAGGACATAGCGTTGGCTACCGTGATATTCCTGAAGAGCTTTGGCGCGATGGG 545
QY      1096  CTGA 1099
Db      546  CTGA 549

RESULT 14
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LOCUS   561 bp      DNA      linear      GSS 08-APR-1999
DEFINITION  mgxb0012101f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0012101f, genomic survey sequence.
ACCESSION AQ447874
VERSION   AQ447874.1 GI:4577011
KEYWORDS GSS.
SOURCE    Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM  Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS   Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 561)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE     A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL   Unpublished (1998)
COMMENT   Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCCTATAGGG
Class: BAC ends
High quality sequence start: 42
High quality sequence stop: 326.
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            /lab_host="E. coli DH10B"
            /clone_lib="CUGI Rice Blast BAC Library"
            /notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
            Rice blast is one of the most devastating fungal diseases
            of rice world wide. It is a filamentous ascomycete with
            a haploid genome (n=7) of approximately 40 Mbp. Rice
            blast is an important model fungal pathogen for studying
            numerous aspects of the fungal-host interaction. In
            order to facilitate genome wide analysis, a BAC library
            containing 9216 clones with an average insert size of 130
            kbp was constructed. This library represents greater
            than 25X genome coverage. High density colony filters
            are available upon request."

ORIGIN
Query Match 6.4%; Score 514.8; DB 8; Length 561;
Best Local Similarity 99.6%; Pred. No. 6.4e-109;
Matches 516; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      510  CAGGGGCGCGCGTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATCACTGCAG 569
Db      44   CAGGGGCGCGCGTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGTTCGAATGCAG 103
QY      570  GACGAGGACGCGCGCTATCGTGGCTGGCCACGACGGCGTTCCTTGGCAGCTGTGCTC 629

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Db      104  GACGAGGACGCGCGCTATCGTGGCTGGCCACGACGCGGCTTCCTTGCAGCTGTGCTC 163
QY      630  GACGTTGTCACTGAAGCGGGAAGGACTGGCTGTCTATTGGGCGAGTGTCCGGGCGAGGAT 689
Db      164  GACGTTGTCACTGAAGCGGGAAGGACTGGCTGTCTATTGGGCGAAGTGTCCGGGCGAGGAT 223
QY      690  CTCCTGTCTATCTCAGCTTGTCTCTCCGAGAAAGATATCCATCATGGCTGATGCAATGCGG 749
Db      224  CTCCTGTCTATCTCAGCTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG 283
QY      750  CGGCTGCATAGCTTGATCCGGCTACCTGCCCATTCGACACCACCAAGCGGAAACATCGCATC 809
Db      284  CGGCTGCATAGCTTGATCCGGCTACCTGCCCATTCGACACCACCAAGCGGAAACATCGCATC 343
QY      810  GAGCGAGCAGCTACTCGGATGGAAGCGGCTCTTGTGCGATCAGGATGATCTGACCAAGAG 869
Db      344  GAGCGAGCAGCTACTCGGATGGAAGCGGCTCTTGTGCGATCAGGATGATCTGACCAAGAG 403
QY      870  CATAGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGGCGCGCATGCCGACGCGC 929
Db      404  CATAGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGGCGCGCATGCCGACGCGC 463
QY      930  GAGGATCTCTGCTGACCCCATGGCGATGCTTGGCGAATATCATGGTGGAAAATGGC 989
Db      464  GAGGATCTCTGCTGACCCCATGGCGATGCTTGGCGAATATCATGGTGGAAAATGGC 523
QY      990  CGCTTTTCTGGATTTCATCGACTGTGGCGGCTGGGCTGT 1027
Db      524  CGCTTTTCTGGATTTCATCGACTGTGGCGGCTGGGCTGT 561

RESULT 15
AQ447775
LOCUS   509 bp      DNA      linear      GSS 08-APR-1999
DEFINITION  mgxb0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0011E13f, genomic survey sequence.
ACCESSION AQ447775
VERSION   AQ447775.1 GI:4576912
KEYWORDS GSS.
SOURCE    Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM  Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS   Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 509)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE     A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL   Unpublished (1998)
COMMENT   Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCCTATAGGG
Class: BAC ends
High quality sequence stop: 342.
FEATURES  Location/Qualifiers
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            /db_xref="taxon:148305"
            /clone="mgxb0011E13f"
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            /lab_host="E. coli DH10B"
            /clone_lib="CUGI Rice Blast BAC Library"
            /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
            Rice blast is one of the most devastating fungal diseases
            of rice world wide. It is a filamentous ascomycete with

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a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

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Query Match          6.4%; Score 508; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.4e-107;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGCGGAAGTCCCGGGCAGGA 688
Db 1 CGACGTTGTCACTGAAGCGGGAAGGAGCTGGCTGCTATTGGCGGAAGTCCCGGGCAGGA 60

Qy 689 TCTCCTGTCACTCACTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATGG 748
Db 61 TCTCCTGTCACTCACTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATGG 120

Qy 749 GCGGCTGCATAGCTGTGATCCGGCTACCTGCCATTCGACCAACAAAGCGAAACATCGCAT 808
Db 121 GCGGCTGCATAGCTGTGATCCGGCTACCTGCCATTCGACCAACAAAGCGAAACATCGCAT 180

Qy 809 CGAGCGAGACGCTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 868
Db 181 CGAGCGAGACGCTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 240

Qy 869 GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCGAGCTCAAGCGCGCATGCCCGACGG 928
Db 241 GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCGAGCTCAAGCGCGCATGCCCGACGG 300

Qy 929 CGAGGATCTCGTGTGACCCATGCGCATGCTTGTCCGGAATATCATGTGGAATAATGG 988
Db 301 CGAGGATCTCGTGTGACCCATGCGCATGCTTGTCCGGAATATCATGTGGAATAATGG 360

Qy 989 CCGCTTTTCTGGATTCAATCGACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048
Db 361 CCGCTTTTCTGGATTCAATCGACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 420

Qy 1049 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCCT 1108
Db 421 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCCT 480

Qy 1109 CGTGTCTTTACGGTATCGCGCTCCCGAT 1136
Db 481 CGTGTCTTTACGGTATCGCGCTCCCGAT 508

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Search completed: November 2, 2004, 06:27:46
Job time : 14586 secs